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From: Stucker, Jeffrey  
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Thanks,  
Jeff Stucker  
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Searcher: AS Kesse, J. G.  
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TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: 1  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST(where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: ABSS02  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_





PA (USSH ) US SEC DEPT HEALTH.  
 XX  
 PI Ahlers JD, Berzofsky JA, Nara P, Pendleton CD, Shirai M;  
 XX WPI; 1995-006707/01.  
 DR  
 XX Polypeptide inducing helper T cell, cytotoxic T cell and  
 PT antibodies responses - to target antigen in hosts of different  
 PT MHC haplotypes, esp. for therapeutic or prophylactic vaccines  
 PT against HIV.  
 XX  
 PS Claim 15; Page 90; 120pp; English.  
 XX  
 CC Synthetic peptides spanning multideterminant regions from the HIV  
 CC envelope protein gp160 have been designed and are designated cluster  
 CC peptides (PCUS). These peptides each consist of a cluster of  
 CC overlapping determinants and are known to induce in vitro T cell  
 CC proliferation and cytokine production in mice and humans of multiple  
 CC MHC types. The cluster peptides were co-linearly synthesised at the  
 CC N-terminus of an immunodominant CTL determinant, Peptide 18, corresp.  
 CC to part of the gp160 V3 loop and principal neutralising determinant  
 CC region. AAR6409 is a specifically claimed example of such a peptide.  
 CC  
 XX  
 SQ Sequence 39 AA;  
 Query Match 100.0%; Score 204; DB 16; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 5e-18;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 KQIINMMQEVGKAMYAPPSGQIRRIQKPGRAVFTIGK 39  
 Db 1 KqIImmQevgkamyapPsgqIrriQpgRafvltIgk 39  
 RESULT 2  
 AAY05339  
 ID AAY05339 standard; peptide; 39 AA.  
 XX  
 AC AAY05339;  
 XX  
 XX 29-JUN-1999 (first entry)  
 DT  
 XX  
 DE HIV-1 CUUVAC peptide; SEQ ID NO. 2.  
 XX  
 KW HIV-1; CUUVAC; cluster peptide vaccine construct; cytotoxic T lymphocyte;  
 KW protective mucosal CTL response; hepatitis A virus; papilloma virus;  
 KW feline immunodeficiency virus; feline leukaemia virus; M. tuberculosis;  
 KW Listeria monocytogenes; M. leprae; Giardia lamblia;  
 KW immune response induction.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX WO9112563-A2.  
 PN  
 XX  
 PD 18-MAR-1999.  
 XX  
 XX  
 PF 11-SEP-1998; 98WO-US19028.  
 PE  
 XX  
 PR 17-FEB-1998; 98US-0074894.  
 PR 11-SEP-1997; 97US-0058523.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
 XX  
 PI Beljakov IM, Berzofsky JA, Derby MA, Kelsall BL;  
 PI Strober W;  
 XX WPI; 1999-243663/20.  
 DR  
 XX Method for inducing a protective mucosal cytotoxic T lymphocyte  
 PT immune response  
 PT  
 PS Claim 21; Page 55; 86pp; English.  
 XX  
 PS

XX This sequence represents a HIV-1 cluster peptide vaccine conjugate  
 CC (CUUVAC) sequence. The invention relates to a method for inducing a  
 CC protective mucosal cytotoxic T lymphocyte (CTL) response in a mammalian  
 CC subject, which comprises contacting a mucosal tissue of the subject with  
 CC a composition comprising a purified soluble antigen. The method can  
 CC induce a protective mucosal CTL response in a subject. The method can  
 CC be used for protection against e.g. hepatitis A virus, papilloma virus,  
 CC feline immunodeficiency virus, feline leukaemia virus, Listeria  
 CC monocytogenes, M. tuberculosis, M. leprae, or Giardia lamblia. The method  
 CC induces long-lasting protective mucosal immune responses.  
 CC  
 XX  
 SQ Sequence 39 AA;  
 Query Match 100.0%; Score 204; DB 20; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 5e-18;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 KQIINMMQEVGKAMYAPPSGQIRRIQKPGRAVFTIGK 39  
 Db 1 KqIImmQevgkamyapPsgqIrriQpgRafvltIgk 39  
 RESULT 3  
 AAR6435  
 ID AAR6435 standard; peptide; 39 AA.  
 XX  
 AC AAR6435;  
 XX  
 XX 03-AUG-1995 (first entry)  
 DT  
 XX  
 DE PCUS 3-18 (421-444) T helper site linked to HIV-1 MN peptide 18.  
 XX  
 KW T cell helper site; cytotoxic T cell response; neutralising antibody;  
 KW human immunodeficiency virus type 1; envelope glycoprotein gp120;  
 KW cluster peptide; principal neutralising determinant.  
 XX  
 OS Synthetic.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..24  
 FT /label= PCUS\_3-18-(421-444)  
 FT /note= "T helper site"  
 FT 25..39  
 FT Region  
 FT /label= peptide\_18  
 FT /note= "corresponds to principal neutralising  
 FT determinant of HIV gp160 V3 loop"  
 XX  
 PN WO9426785-A.  
 XX  
 XX 24-NOV-1994.  
 PD  
 XX  
 XX 13-MAY-1994; 94WO-US05142.  
 PF  
 XX  
 PR 14-MAY-1993; 93US-0060988.  
 PR  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (USSH ) US SEC DEPT HEALTH.  
 XX  
 PI Ahlers JD, Berzofsky JA, Nara P, Pendleton CD, Shirai M;  
 XX WPI; 1995-006707/01.  
 DR  
 XX Polypeptide inducing helper T cell, cytotoxic T cell and  
 PT antibodies responses - to target antigen in hosts of different  
 PT MHC haplotypes, esp. for therapeutic or prophylactic vaccines  
 PT against HIV.  
 XX  
 PS Claim 15; Page 90; 120pp; English.  
 XX  
 CC Synthetic peptides spanning multideterminant regions from the HIV  
 CC envelope protein gp160 have been designed and are designated cluster

CC peptides (PClUS). These peptides each consist of a cluster of  
 CC overlapping determinants and are known to induce in vitro T cell  
 CC proliferation and cytokine production in mice and humans of multiple  
 CC MHC types. The cluster peptides were co-linearly synthesized at the  
 CC N-terminus of an immunodominant CTL determinant. Peptide 18, corresp.  
 CC to part of the gp160 V3 loop and principal neutralising determinant  
 CC region. AAR66435 is a specifically claimed example of such a peptide.  
 XX  
 SQ Sequence 39 AA;

Query Match 83.8%; Score 171; DB 16; Length 39;  
 Best Local Similarity 91.7%; Pred. No. 5e-14;  
 Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 KOIINMGEVGRKAMVAPISQIRIRIQPGRAVFT 36  
 |||||||  
 DB 1 KqIImwgevGRKAMVAPISQIRIRIRIQPGRAVFT 36

## RESULT 4

AAV05346  
 ID AAV05346 standard; peptide; 39 AA.

AC AAV05346;

DT 29-JUN-1999 (first entry)

DE HIV-1 CLUVAC peptide, SEQ ID NO. 9.

XX HIV-1 CLUVAC; cluster peptide vaccine construct; cytotoxic T lymphocyte;

KM protective mucosal CTL response; hepatitis A virus; papilloma virus;

KM feline immunodeficiency virus; feline leukemia virus; M. tuberculosis;

KM Listeria monocytogenes; M. leprae; Giardia lamblia;

XX immune response induction.

XX Human immunodeficiency virus type 1.

XX WO9912563-A2.

XX 18-MAR-1999.

XX 11-SEP-1998; 98WO-US19028.

XX 17-FEB-1998; 98US-0074894.

XX 11-SEP-1997; 97US-0058523.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICE.

XX Beljakov IM, Berzofsky JA, Derby MA, Kelsall BL;

XX Strober W;

XX WPI, 1999-243663/20.

XX Method for inducing a protective mucosal cytotoxic T lymphocyte

XX immune response

XX Claim 21; Page 55; 86pp; English.

XX This sequence represents a HIV-1 cluster peptide vaccine conjugate

CC (CLUVAC) sequence. The invention relates to a method for inducing a

CC protective mucosal cytotoxic T lymphocyte (CTL) response in a mammalian

CC subject, which comprises contacting a mucosal tissue of the subject with

CC a composition comprising a purified soluble antigen. The method can

CC induce a protective mucosal CTL response in a subject. The method can be

CC used for protection against e.g. hepatitis A virus, papilloma virus,

CC feline immunodeficiency virus, feline leukemia virus, Listeria

CC monocytogenes, M. tuberculosis, M. leprae, or Giardia lamblia. The method

CC induces long-lasting protective mucosal immune responses.

XX Sequence 39 AA;

Query Match 83.8%; Score 171; DB 20; Length 39;  
 Best Local Similarity 91.7%; Pred. No. 5e-14;  
 Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 KOIINMGEVGRKAMVAPISQIRIRIQPGRAVFT 36  
 |||||||  
 DB 1 KqIImwgevGRKAMVAPISQIRIRIRIQPGRAVFT 36

## RESULT 5

AAR58552  
 ID AAR58552 standard; Protein; 150 AA.

AC AAR58552;

DT 29-MAR-1995 (first entry)

DE MEAV vaccine.

XX HIV-1; V3 loop; multiple epitope; AIDS; vaccine; MEAV;

XX Escherichia coli; PKR-MEAV.

XX Synthetic.

XX Key Location/Qualifiers

FT Domain 1..29 /label= CD4\_binding\_domain

FT Peptide 30..35 /label= Spacer

FT Peptide 36..51 /label= MN\_peptide

FT Peptide 52..57 /note= "peptide from V3 loop of HIV-1 isolate MN"

FT Peptide 58..73 /label= Spacer

FT Peptide 74..79 /label= SC\_peptide

FT Peptide 80..97 /note= "peptide from V3 loop of HIV-1 isolate SC"

FT Peptide 98..103 /label= RF\_peptide

FT Peptide 104..121 /note= "peptide from V3 loop of HIV-1 isolate RF"

FT Peptide 122..127 /label= Spacer

FT Peptide 128..142 /label= IIIB\_peptide

FT Peptide 143..148 /note= "peptide from V3 loop of HIV-1 isolate IIIB"

FT Peptide 149..163 /label= Spacer

XX WO9418234-A.

XX 18-AUG-1994.

XX 10-FEB-1994; 94WO-US01523.

XX 10-FEB-1993; 93US-0015770.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Shen DF, Wang CY;

XX WPI, 1994-279687/34.

XX N-PsDB; AA070535.

XX New recombinant proteins contg multiple antigenic determinants -

XX linked by flexible hinge domains

XX

PS Disclosure: Page 37-38; 56pp; English.

XX MEAV gene encodes a portion of the CD4 binding domain (AAR58550)

CC of HIV env protein, the domain being capable of inducing a helper T-

CC cell response, and 5 peptide domains from the V3 loop of HIV-1

CC isolates MN, SC, RF, IIB and WMJ2 (AAR58545-49), each peptide being

CC separated by a spacer domain (AAR58551). The gene was expressed in E.

CC coli BL21/pKK-MEAV for preparation of a multiple epitope AIDS

CC vaccine.

XX

SO Sequence 150 AA;

Query Match 76.2%; Score 155.5; DB 15; Length 150;

Best Local Similarity 71.1%; Pred. No. 1.3e-11;

Matches 32; Conservative 1; Mismatches 3; Indels 9; Gaps 1;

OY 1 KQIINMDEVCAMYPAPISQIR-----RIORGGRAFVIT 36

DB 4 kgIIMMGEVgKAMyrpIISgIrcdppdpkrlhIpgpgrafvIt 48

RESULT 6

AKM32953

ID AAM32953 standard; peptide: 41 AA.

XX

AC AAM32953;

XX

DT 23-JAN-1998 (first entry)

XX

DE C3-V3 LAI immunogen construct.

XX

KW Immunogen: antigenic determinant; HIV: envelope; glycoprotein;

KW env; gp; recognition; B lymphocyte; type specific; antibody;

KW vaccine; protection; immune response; infection; neutralisation.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

PN WO9714436-A1.

XX

PD 24-APR-1997.

XX

PE 18-OCT-1996; 96WO-US16911.

XX

PR 09-FEB-1996; 96US-0599266.

PR 20-OCT-1995; 95US-0546515.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Haynes BF, Parker TJ;

XX

DR WPI: 1997-244862/22.

XX

PT Synthetic human immunodeficiency virus vaccine - comprising

PT hydrophilic peptide corresponding to at least 1 antigenic

PT determinant of envelope glyco:protein recognised by B lymphocytes

XX

PS Example 11; Page 60j; 104pp; English.

XX

SO Sequence 41 AA;

XX

CC The present sequence, which comprises at least 1 antigenic

CC determinant of human immunodeficiency virus (HIV) envelope (env)

CC glycoprotein (gp) recognised by B lymphocytes, when covalently

CC linked to a carrier molecule, induces the production of high

CC titres of protective, type specific anti-HIV antibodies (Ab) in a

CC mammal. The peptide can be used in vaccines for producing a

CC neutralising immune response to HIV infection, while a HIV

CC neutralising Ab can be induced in a primate by administering a

CC composition comprising HIV env peptides that disrupt gp120/gp41

CC interactions.

XX

SO Sequence 41 AA;

Query Match 68.9%; Score 140.5; DB 18; Length 41;

Best Local Similarity 73.2%; Pred. No. 2.6e-10;

Matches 30; Conservative 1; Mismatches 7; Indels 3; Gaps 1;

OY 1 KQIINMDEVCAMYPAPISQIR-----RIORGGRAFVITG 38

DB 1 kgIIMMGEVgKAMyrpIISgIrcdppdpkrlhIpgpgrafvItg 41

RESULT 7

AKM32954

ID AAM32954 standard; peptide: 41 AA.

XX

AC AAM32954;

XX

DT 23-JAN-1998 (first entry)

XX

DE C3-V3 HXB2R immunogen construct.

XX

KW Immunogen: antigenic determinant; HIV: envelope; glycoprotein;

KW env; gp; recognition; B lymphocyte; type specific; antibody;

KW vaccine; protection; immune response; infection; neutralisation.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

PN WO9714436-A1.

XX

PD 24-APR-1997.

XX

PE 18-OCT-1996; 96WO-US16911.

XX

PR 09-FEB-1996; 96US-0599266.

PR 20-OCT-1995; 95US-0546515.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Haynes BF, Parker TJ;

XX

DR WPI: 1997-244862/22.

XX

PT Synthetic human immunodeficiency virus vaccine - comprising

PT hydrophilic peptide corresponding to at least 1 antigenic

PT determinant of envelope glyco:protein recognised by B lymphocytes

XX

PS Example 11; Page 60j; 104pp; English.

XX

SO Sequence 41 AA;

XX

CC The present sequence, which comprises at least 1 antigenic

CC determinant of human immunodeficiency virus (HIV) envelope (env)

CC glycoprotein (gp) recognised by B lymphocytes, when covalently

CC linked to a carrier molecule, induces the production of high

CC titres of protective, type specific anti-HIV antibodies (Ab) in a

CC mammal. The peptide can be used in vaccines for producing a

CC neutralising immune response to HIV infection, while a HIV

CC neutralising Ab can be induced in a primate by administering a

CC composition comprising HIV env peptides that disrupt gp120/gp41

CC interactions.

XX

SO Sequence 41 AA;

```

ID AAM32955 standard; peptide: 41 AA.
XX
AC AAM32955;
XX
DT 23-JAN-1998 (first entry)
XX
DE C3-V3 NL43 immunogen construct.
XX
KM Immunogen: antigenic determinant; HIV; envelope; glycoprotein;
KM env; gp; recognition; B lymphocyte; type specific; antibody;
KM vaccine; protection; immune response; infection; neutralisation.
XX
OS Human immunodeficiency virus.
OS Synthetic.
PN WO9714436-A1.
PD 24-APR-1997.
XX
PF 18-OCT-1996; 96WO-US16911.
XX
PR 09-FEB-1996; 96US-0599266.
XX
PR 20-OCT-1995; 95US-0546515.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Palker TJ;
XX
DR WPI: 1997-244862/22.
XX
PT Synthetic human immunodeficiency virus vaccine - comprising
PT hydrophilic peptide corresponding to at least 1 antigenic
PT determinant of envelope glyco:protein recognised by B lymphocytes
XX
PS Example 11; Page 603; 104pp; English.
XX
CC The present sequence, which comprises at least 1 antigenic
CC determinant of human immunodeficiency virus (HIV) envelope (env)
CC glycoprotein (gp) recognised by B lymphocytes, when covalently
CC linked to a carrier molecule, induces the production of high
CC titres of protective, type specific anti-HIV antibodies (Ab) in a
CC mammal. The peptide can be used in vaccines for producing a
CC protective immune response to HIV infection, while a HIV
CC neutralising Ab can be induced in a primate by administering a
CC composition comprising HIV env peptides that disrupt gp120/gp41
CC interactions.
XX
SQ Sequence 41 AA;

```

```

Query Match 68.9%; Score 140.5; DB 18; Length 41;
Best Local Similarity 73.2%; Pred. No. 2.6e-10;
Matches 30; Conservative 1; Mismatches 7; Indels 3; Gaps 1;
OY 1 KOINMMQEVGKAMYAPISQIR--RIORGPGRFVITG 38
  ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 kqfinmwgevgkamypatrrpnntkksirirgprafvlig 41

```

```

RESULT 9
ID AAM32956 standard; peptide: 41 AA.
XX
AC AAM32956;
XX
DT 23-JAN-1998 (first entry)
XX
DE C3-V3 MFA immunogen construct.
XX
KM Immunogen: antigenic determinant; HIV; envelope; glycoprotein;
KM env; gp; recognition; B lymphocyte; type specific; antibody;
KM vaccine; protection; immune response; infection; neutralisation.
XX

```

```

OS Human immunodeficiency virus.
OS Synthetic.
PN WO9714436-A1.
PD 24-APR-1997.
XX
PF 18-OCT-1996; 96WO-US16911.
XX
PR 09-FEB-1996; 96US-0599266.
XX
PR 20-OCT-1995; 95US-0546515.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Palker TJ;
XX
DR WPI: 1997-244862/22.
XX
PT Synthetic human immunodeficiency virus vaccine - comprising
PT hydrophilic peptide corresponding to at least 1 antigenic
PT determinant of envelope glyco:protein recognised by B lymphocytes
XX
PS Example 11; Page 603; 104pp; English.
XX
CC The present sequence, which comprises at least 1 antigenic
CC determinant of human immunodeficiency virus (HIV) envelope (env)
CC glycoprotein (gp) recognised by B lymphocytes, when covalently
CC linked to a carrier molecule, induces the production of high
CC titres of protective, type specific anti-HIV antibodies (Ab) in a
CC mammal. The peptide can be used in vaccines for producing a
CC protective immune response to HIV infection, while a HIV
CC neutralising Ab can be induced in a primate by administering a
CC composition comprising HIV env peptides that disrupt gp120/gp41
CC interactions.
XX
SQ Sequence 41 AA;

```

```

Query Match 68.9%; Score 140.5; DB 18; Length 41;
Best Local Similarity 73.2%; Pred. No. 2.6e-10;
Matches 30; Conservative 1; Mismatches 7; Indels 3; Gaps 1;
OY 1 KOINMMQEVGKAMYAPISQIR--RIORGPGRFVITG 38
  ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 kqfinmwgevgkamypatrrpnntkksirirgprafvlig 41

```

```

RESULT 10
ID AAR40194 standard; peptide: 41 AA.
XX
AC AAR40194;
XX
DT 05-FEB-1994 (first entry)
XX
DE Sequence of peptide construct T1-SP10IIR(A), type Th-B,
DE derived from HIV MN and HIVIIR Env gp120.
XX
KM Hybrid protein; synthetic protein; immunogenic peptide; tolerance;
KM synthetic toleragen.
XX
OS Synthetic.
XX
PN WO9315750-A.
XX
PD 19-AUG-1993.
XX
PF 10-FEB-1993; 93WO-US01207.
XX
PR 10-FEB-1992; 92US-0833429.
XX
PA (HAYN/) HAYNES B F.
XX

```

PI Haynes BF;  
 XX  
 DR WPI: 1993-272554/34.  
 XX  
 PT Inducing immune tolerance to immunogenic peptide(s) or proteins -  
 PT by administering the peptide(s) or proteins coupled to a 2-20  
 PT aminoacid hydrophobic peptide  
 XX  
 PS Example: Table 8, page 42; 65pp; English.  
 XX  
 CC The peptide composition and sequence (epitope type) of the  
 CC synthetic peptide construct is T1(Th) SP10(B cell) and A(B cell).  
 CC T1 sequence is Aas 428-443 from HIVIIIB.  
 CC SP10IIIB is Aas 303-321 from HIVIIIB.  
 CC (A) sequence is Aas 320-324 from HIVM and Aas 322-327 from HIVIIIB.  
 CC Th = T helper cell determinant.  
 CC B cell = B cell neutralising antibody determinant.  
 XX  
 SQ Sequence 41 AA:  
 SQ

Query Match 63.7%; Score 130; DB 14; Length 41;  
 Best Local Similarity 73.2%; Pred. No. 4.9e-09;  
 Matches 30; Conservative 2; Mismatches 5; Indels 4; Gaps 2;

OY 1 KOIINMGEVKGAMVA--PPISQIR--RIORGGRAFYTI 37  
 DB 1 KqIINMGEVKGAMVactrpnntkrsIrlqrpgrafvltl 41

RESULT 11  
 ID AAY04026  
 AC AAY04026;  
 XX  
 DT 20-DEC-1999 (first entry)  
 XX  
 DE HIV peptide T1-SP10IIIB(A) for use in immunogenic complex.  
 XX  
 KW Macroglobulin: HIV: immunogenic complex; human immunodeficiency virus;  
 KW hepatitis; antigen; vaccine.  
 OS  
 XX Human immunodeficiency virus.  
 XX  
 PN WO950303-A2.  
 PD 07-OCT-1999.  
 XX  
 PE 01-APR-1999: 99WO-US07236.  
 XX  
 PR 01-APR-1998: 98US-0053301.  
 PR 31-MAR-1999: 99US-0053301.  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Pizzo SV, Gron H;  
 XX  
 DR WPI: 1999-601324/51.  
 XX  
 PT Immune response modulator alpha-2 macroglobulin complex useful in the  
 PT treatment of HIV or hepatitis -  
 XX  
 PS Claim 3; Page 77; 103pp; English.  
 XX  
 CC A stable complex comprising at least one intact biomolecule and  
 CC activated alpha-2-macroglobulin (alpha-2M) having an intact bait  
 CC region is claimed, in which the biomolecule is covalently bound to  
 CC an amino acid residue of a cleaved thiol ester of the alpha-2M,  
 CC the amino acid residue being a glutamyl residue and/or a cysteinyl  
 CC residue. Preparation of the complex comprises activation of alpha-2M  
 CC with a nucleophilic compound followed by incubation with the  
 CC biomolecule at elevated temperature. Covalent incorporation of the

CC intact biomolecule is thus effected without use of a protease. The  
 CC obtained complex may be used as an antigen for stimulating immune  
 CC response, e.g. in the form of a vaccine. Enhanced presentation of the  
 CC biomolecule is provided, especially for those antigens which are poorly  
 CC immunogenic. Reduction of immunodominance of particular epitopes is  
 CC also provided. Preferably the biomolecule is an HIV antigen or a  
 CC hepatitis virus antigen, or a peptide, fragment, hybrid or chimeric  
 CC peptide thereof. The present sequence is a preferred example of an HIV  
 CC peptide which may be used in the complex.  
 XX  
 SQ Sequence 41 AA:  
 SQ

Query Match 63.7%; Score 130; DB 20; Length 41;  
 Best Local Similarity 73.2%; Pred. No. 4.9e-09;  
 Matches 30; Conservative 2; Mismatches 5; Indels 4; Gaps 2;

OY 1 KOIINMGEVKGAMVA--PPISQIR--RIORGGRAFYTI 37  
 DB 1 KqIINMGEVKGAMVactrpnntkrsIrlqrpgrafvltl 41

RESULT 12  
 ID AAR40193  
 AC AAR40193;  
 XX  
 DT 05-FEB-1994 (first entry)  
 XX  
 DE Sequence of peptide construct F-T1-SP10IIIB(A), type F-Th-B,  
 DE derived from HIV MN and HIVIIIB Env gp120.  
 XX  
 KW Hybrid protein: synthetic protein; immunogenic peptide; tolerance;  
 KW synthetic toleragen.  
 OS  
 XX Synthetic.  
 XX  
 PN WO9315750-A.  
 PD 19-AUG-1993.  
 XX  
 PE 10-FEB-1993: 93WO-US01207.  
 XX  
 PR 10-FEB-1992: 92US-0833429.  
 PA (HAYN/) HAYNES B F.  
 XX  
 PI Haynes BF;  
 XX  
 DR WPI: 1993-272554/34.  
 XX  
 PT Inducing immune tolerance to immunogenic peptide(s) or proteins -  
 PT by administering the peptide(s) or proteins coupled to a 2-20  
 PT aminoacid hydrophobic peptide  
 XX  
 PS Example: Table 8, page 42; 65pp; English.  
 XX  
 CC The peptide composition and sequence (epitope type) of the  
 CC synthetic peptide construct is F-T1(Th) SP10(B cell) and A(B  
 CC cell). T1 sequence is Aas 428-443 from HIVIIIB.  
 CC SP00IIIB sequences is Aas 303-321 from HIVIIIB.  
 CC (A) sequence is Aas 320-324 from HIVM and Aas 322-327 from HIVIIIB.  
 CC Th = T helper cell determinant.  
 CC B cell = B cell neutralising antibody determinant. A = additional  
 CC HIV gp120 V3 loop sequences added to the original synthetic peptide  
 CC (SP10) sequence to add an additional neutralising and CTL region  
 CC to the HIV B cell determinant of the hybrid peptide. F (Immunogenic  
 CC domain) sequence is Aas 519-530 from HIVIIIB.  
 XX  
 SQ Sequence 53 AA:



Query Match 63.7%; Score 130; DB 14; Length 53;  
 Best Local Similarity 73.2%; Pred. No. 6.2e-09;  
 Matches 30; Conservative 2; Mismatches 5; Indels 4; Gaps 2;

OY 1 KOIIMMOEYKAMYA--PISGOIR--RIORGGRFAFVTI 37  
 |||||  
 DB 13 KqIIMMGEVgkamyactrpnntkrksirIdrgprafvltl 53

RESULT 13  
 AAM16534

ID AAM16534 standard; peptide: 53 AA.

XX AAM16534;

XX 14-JAN-1998 (first entry)

DE Peptide (F-T1-SPL0(A)) comprising HIV antigenic determinant.

KM Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein;

KW env; gp; recognition; B lymphocyte; type specific; antibody;

XX vaccine; protection; immune response; infection; neutralisation.

OS Human immunodeficiency virus.

XX W09714436-A1.

XX 24-APR-1997.

XX 18-OCT-1996; 96WO-US16911.

XX 09-FEB-1996; 96US-0599266.

XX 20-OCT-1995; 95US-0546515.

XX (UYDU-) UNIV DUKE.

XX Haynes BF, Parker TJ;

XX WPI: 1997-244862/22.

PT Synthetic human immunodeficiency virus vaccine - comprising  
 hydrophilic peptide corresponding to at least 1 antigenic  
 determinant of envelope glyco:protein recognised by B lymphocytes

XX Disclosure: Page 18; 104pp; English.

XX An essentially pure hydrophilic peptide, i.e. the present peptide,  
 comprising at least 1 antigenic determinant of human

CC immunodeficiency virus (HIV) envelope (env) glycoprotein (gp)

CC recognised by B lymphocytes, when covalently linked to a carrier

CC molecule induces the production of high titres of protective, type

CC specific anti-HIV antibodies (Ab) in a mammal. The peptide can be

CC used in vaccines for producing a protective immune response to HIV

CC infection, while a HIV neutralising Ab can be induced in a primate

CC by administering a composition comprising HIV env peptides that

CC disrupt gp120/gp41 interactions.

XX Sequence 53 AA;

XX Query Match 63.7%; Score 130; DB 18; Length 53;

XX Best Local Similarity 73.2%; Pred. No. 6.2e-09;

XX Matches 30; Conservative 2; Mismatches 5; Indels 4; Gaps 2;

OY 1 KOIIMMOEYKAMYA--PISGOIR--RIORGGRFAFVTI 37  
 |||||  
 DB 13 KqIIMMGEVgkamyactrpnntkrksirIdrgprafvltl 53

RESULT 14  
 AAP94802

XX ID AAP94802 standard; protein: 229 AA.

AC AAP94802;  
 XX 22-JUN-1990 (first entry)  
 DT  
 XX  
 DE PBlrf HIV fusion protein.  
 XX  
 KW HIV; AIDS; PBlrf fusion protein; HIV vaccine; ds.

XX HIV.

OS Key Location/Qualifiers

XX Key Protein 31..156

FT Protein /label= HIV derived sequence

XX EP306219-A.

XX 08-MAR-1989.

XX 25-AUG-1988; 88EP-0307889.

XX 25-AUG-1988; 88EP-0307889.

XX (REPL-) REPLIGEN CORP.

XX Rusche JR, Putney SD, Javaherian K, Farley J, Grimalia R, Lynn D;

XX Petro J, O'Keefe T;

XX WPI: 1989-070387/10.

XX N-PSDB; AAN90627.

XX New HIV proteins and peptide(s) -

XX used in diagnosis, prophylaxis or therapy of AIDS esp. for

XX prep. of vaccines against HIV infection.

XX Claim 1; Table 4; 29pp; English.

XX Protein derivative stimulates a lymphocyte proliferative response in

XX HIV-infected humans, providing a means of diagnosis, protection and

XX therapeutic value.

XX Sequence 229 AA;

OY 1 KOIIMMOEYKAMYPAPISGOIRRIORGGRFAFVTIG 38  
 |||||

DB 158 KqIIVMMGEVgkamyappisgqikcistnltglllttdg 195

RESULT 15  
 AAR33837

ID AAR33837 standard; peptide: 24 AA.

XX AAR33837;

XX 13-JUL-1993 (first entry)

XX Cluster peptide PCLUS3.

XX Multideterminant; cluster; HIV; envelope protein; T-cell; mice; MHC;

XX human; T lymphocyte; HLA; vaccine.

XX Synthetic.

XX W09304697-A.

XX 18-MAR-1993.

XX 31-AUG-1992; 92WO-US07422.

29-AUG-1991: 910S-0751998.  
(USSH ) US DEPT HEALTH & HUMAN SERVICE.  
Berzofsky JA;  
WPI; 1993-100657/12.  
Multi-determinant peptide antigens - stimulate T-helper response against HIV, for treating and diagnosing HIV infection  
Claim 7; Page 28; 37pp; English.  
The sequences given in AAR33835-40 are peptides which encompass multi-determinant clusters of HIV envelope protein that induce in vitro T-cell response in mice of multiple MHC type and in a population of HIV seropositive humans. These peptides stimulate helper T lymphocyte response to HIV in humans of many HLA types. They can be used for the diagnosis or prognosis of HIV, for the production of vaccines or for the therapeutic treatment of HIV infection.

Query	Match	Similarity	Best Local	Score	127	DB	14	Length	24
				62.3%					
				100.0%					
Matches	24	Conservative	0	Mismatches	0	Indels	0	Gaps	0
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Db	1	KqIImMwEvGvKAmYApPISgIr	24						

Search completed: January 2, 2002, 09:57:22  
job time: 52 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 2, 2002, 09:56:30 ; Search time 12.45 seconds  
(without alignments)  
70.492 Million cell updates/sec

Title: US-09-508-552-2

Sequence: 204  
1 KQINMWDEVGRAMYPISQIRRIQSGPRAFTIGK 39

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	39	2 US-08-455-625-2	Sequence 2, Appl1
2	204	100.0	39	4 US-08-455-685-2	Sequence 2, Appl1
3	204	100.0	39	4 US-08-060-988A-2	Sequence 2, Appl1
4	204	100.0	39	5 PCT-US94-05142-2	Sequence 2, Appl1
5	171	83.8	39	2 US-08-455-625-28	Sequence 28, Appl1
6	171	83.8	39	4 US-08-455-685-28	Sequence 28, Appl1
7	171	83.8	39	4 US-08-060-988A-28	Sequence 28, Appl1
8	171	83.8	39	5 PCT-US94-05142-28	Sequence 28, Appl1
9	146.5	71.8	130	1 US-08-015-770B-8	Sequence 8, Appl1
10	127	62.3	24	2 US-08-455-625-24	Sequence 24, Appl1
11	127	62.3	24	2 US-08-407-252-3	Sequence 3, Appl1
12	127	62.3	24	4 US-08-455-685-24	Sequence 24, Appl1
13	127	62.3	24	4 US-08-060-988A-24	Sequence 24, Appl1
14	127	62.3	24	5 PCT-US94-05142-24	Sequence 24, Appl1
15	127	62.3	28	1 US-08-488-252-1	Sequence 1, Appl1
16	127	62.3	28	2 US-08-448-603A-12	Sequence 12, Appl1
17	127	62.3	28	5 US-09-134-075-12	Sequence 12, Appl1
18	127	62.3	28	5 PCT-US92-06688-1	Sequence 1, Appl1
19	127	62.3	181	5 PCT-US93-07805-1	Sequence 1, Appl1
20	127	62.3	496	5 US-08-889-841B-12	Sequence 12, Appl1
21	127	62.3	496	4 US-08-889-841B-16	Sequence 16, Appl1
22	127	62.3	856	4 US-09-124-900-9	Sequence 9, Appl1
23	127	62.3	863	3 US-08-463-210-11	Sequence 11, Appl1
24	127	62.3	880	2 US-08-788-815-7	Sequence 7, Appl1
25	127	62.3	880	3 US-09-157-963-7	Sequence 7, Appl1
26	125	61.3	519	4 US-08-472-240A-18	Sequence 18, Appl1
27	125	61.3	865	4 US-07-956-483-13	Sequence 13, Appl1

28	125	61.3	887	4 US-08-472-240A-4	Sequence 4, Appl1
29	123	60.3	27	2 US-08-493-235-34	Sequence 34, Appl1
30	123	60.3	28	1 US-08-488-252-2	Sequence 2, Appl1
31	123	60.3	28	1 US-08-488-252-3	Sequence 3, Appl1
32	123	60.3	28	1 US-08-488-252-6	Sequence 6, Appl1
33	123	60.3	28	1 US-08-488-252-7	Sequence 7, Appl1
34	123	60.3	28	2 US-08-448-603A-4	Sequence 4, Appl1
35	123	60.3	28	2 US-08-448-603A-5	Sequence 5, Appl1
36	123	60.3	28	2 US-08-448-603A-10	Sequence 10, Appl1
37	123	60.3	28	2 US-08-448-603A-11	Sequence 11, Appl1
38	123	60.3	28	2 US-08-448-603A-13	Sequence 13, Appl1
39	123	60.3	28	2 US-08-448-603A-15	Sequence 15, Appl1
40	123	60.3	28	2 US-08-448-603A-21	Sequence 21, Appl1
41	123	60.3	28	3 US-09-134-075-4	Sequence 4, Appl1
42	123	60.3	28	3 US-09-134-075-5	Sequence 5, Appl1
43	123	60.3	28	3 US-09-134-075-10	Sequence 10, Appl1
44	123	60.3	28	3 US-09-134-075-11	Sequence 11, Appl1
45	123	60.3	28	3 US-09-134-075-13	Sequence 13, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-455-625-2  
; Sequence 2, Application US/08455625  
; Patent No. 5932218  
; GENERAL INFORMATION:  
; APPLICANT: Berzofsky, Jay A.  
; APPLICANT: Ahlers, Jeffrey D.  
; APPLICANT: Pendleton, C. D.  
; APPLICANT: Nara, Peter  
; APPLICANT: Shiral, Mutsumori  
; TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT  
; TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T  
; TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,625  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/060,988  
; FILING DATE: 14-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svensson, Leonard R.  
; REGISTRATION NUMBER: 30330  
; REFERENCE/DOCKET NUMBER: 1173-434P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-205-8000  
; TELEFAX: 703-205-8050  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: Internal  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..39

OTHER INFORMATION: /label= peptide  
OTHER INFORMATION: /note= "pctus 3-18/p181iib peptide, see Table 1"  
US-08-455-625-2

Query Match 100.0%; Score 204; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 5.7e-22;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOEYKAMYPAPISQIRIRIOGPGRAFTVIGK 39  
DB 1 KOIINMOEYKAMYPAPISQIRIRIOGPGRAFTVIGK 39

## RESULT 2

US-08-455-685-2  
Sequence 2, Application US/08455685  
Patent No. 6214347  
GENERAL INFORMATION:  
APPLICANT: Berzolsky, Jay A.  
APPLICANT: Ahlers, Jeffrey D.  
APPLICANT: Pendleton, C. David  
APPLICANT: Nara, Peter  
APPLICANT: Shirai, Mutsumori  
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES THAT ELICIT  
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND  
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,685  
FILING DATE: 31-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/060,988  
FILING DATE: 14-MAY-1993  
APPLICATION NUMBER: 07/847,311  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/751,998  
FILING DATE: 29-AUG-1991  
APPLICATION NUMBER: 07/148,692  
FILING DATE: 26-JAN-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Beattie, Ingrid A.  
REGISTRATION NUMBER: P-42,306  
REFERENCE/DOCKET NUMBER: 08830/022003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-455-685-2

Query Match 100.0%; Score 204; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 5.7e-22;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOEYKAMYPAPISQIRIRIOGPGRAFTVIGK 39  
DB 1 KOIINMOEYKAMYPAPISQIRIRIOGPGRAFTVIGK 39

## RESULT 3

US-08-060-988A-2  
Sequence 2, Application US/08060988A  
Patent No. 6294322  
GENERAL INFORMATION:  
APPLICANT: Berzolsky, Jay A.  
APPLICANT: Ahlers, Jeffrey D.  
APPLICANT: Pendleton, C. David  
APPLICANT: Nara, Peter  
APPLICANT: Shirai, Mutsumori  
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES  
TITLE OF INVENTION: THAT ELICIT  
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND  
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/060,988A  
FILING DATE: 14-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/847,311  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/751,998  
FILING DATE: 29-AUG-1991  
APPLICATION NUMBER: 07/148,692  
FILING DATE: 26-JAN-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Beattie, Ingrid A.  
REGISTRATION NUMBER: P-42,306  
REFERENCE/DOCKET NUMBER: 08830/022001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-060-988A-2

Query Match 100.0%; Score 204; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 5.7e-22;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOEYKAMYPAPISQIRIRIOGPGRAFTVIGK 39  
DB 1 KOIINMOEYKAMYPAPISQIRIRIOGPGRAFTVIGK 39

## RESULT 4

PCT-US94-05142-2  
Sequence 2, Application PC/TUS9405142  
GENERAL INFORMATION:  
APPLICANT:

;; TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT  
;; TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T  
;; TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV  
;; NUMBER OF SEQUENCES: 36  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
;; STREET: P.O. Box 747  
;; CITY: Falls Church  
;; STATE: Virginia  
;; COUNTRY: USA  
;; ZIP: 22040-0747  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US94/05142  
;; FILING DATE: 13-MAY-1994  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/060,988  
;; FILING DATE: 14-MAY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Svensson, Leonard R.  
;; REGISTRATION NUMBER: 30330  
;; REFERENCE/DOCKET NUMBER: 1173-434P  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-205-8000  
;; TELEFAX: 703-205-8050  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 39 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..39  
;; OTHER INFORMATION: /label= peptide  
;; OTHER INFORMATION: /note="pclus 3-18/p18ITIB peptide, see Table 1"  
PCT-US94-05142-2

Query Match 100.0%; Score 204; DB 5; Length 39;  
Best Local Similarity 100.0%; Pred. No. 5.7e-22;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIIMMGEVGKAMVAPISGQIRIRIOPGPAFTICK 39  
DB 1 KOIIMMGEVGKAMVAPISGQIRIRIOPGPAFTICK 39

RESULT 5  
US-08-455-625-28  
Sequence 28, Application US/08455625  
Patent No. 5932218  
GENERAL INFORMATION:  
APPLICANT: Berzofsky, Jay A.  
APPLICANT: Ahlers, Jeffrey D.  
APPLICANT: Pendleton, C. D.  
APPLICANT: Nara, Peter  
APPLICANT: Shirai, Mutsunori  
TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT  
TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T  
TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: Virginia

;; COUNTRY: USA  
;; ZIP: 22040-0747  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/455,625  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/060,988  
;; FILING DATE: 14-MAY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Svensson, Leonard R.  
;; REGISTRATION NUMBER: 30330  
;; REFERENCE/DOCKET NUMBER: 1173-434P  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-205-8000  
;; TELEFAX: 703-205-8050  
;; INFORMATION FOR SEQ ID NO: 28:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 39 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..39  
;; OTHER INFORMATION: /label= peptide  
;; OTHER INFORMATION: /note="pclus3-18MN peptide, see Table VI"  
US-08-455-625-28

Query Match 83.8%; Score 171; DB 2; Length 39;  
Best Local Similarity 91.7%; Pred. No. 2.3e-17;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOIIMMGEVGKAMVAPISGQIRIRIOPGPAFT 36  
DB 1 KOIIMMGEVGKAMVAPISGQIRIRIOPGPAFT 36

RESULT 6  
US-08-455-685-28  
Sequence 28, Application US/08455685  
Patent No. 6214347  
GENERAL INFORMATION:  
APPLICANT: Berzofsky, Jay A.  
APPLICANT: Ahlers, Jeffrey D.  
APPLICANT: Pendleton, C. David  
APPLICANT: Nara, Peter  
APPLICANT: Shirai, Mutsunori  
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES THAT ELICIT  
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND  
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,685

FILED DATE: 31-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/060,988  
FILING DATE: 14-MAY-1993  
APPLICATION NUMBER: 07/847,311  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/751,998  
FILING DATE: 29-AUG-1991  
APPLICATION NUMBER: 07/148,692  
FILING DATE: 26-JAN-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Beattie, Ingrid A.  
REGISTRATION NUMBER: P-42,306  
REFERENCE/DOCKET NUMBER: 08830/022003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-455-685-28

Query Match 83.8%; Score 171; DB 4; Length 39;  
Best Local Similarity 91.7%; Pred. No. 2.3e-17;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KQIINMDEVKAMYPISQIRIRHIGPGRAFT 36  
Db 1 KQIINMDEVKAMYPISQIRIRHIGPGRAFT 36

RESULT 7  
US-08-060-988A-28  
Sequence 28, Application US/08060988A  
Patent No. 6294322  
GENERAL INFORMATION:  
APPLICANT: Berzofsky, Jay A.  
APPLICANT: Abiers, Jeffrey D.  
APPLICANT: Pendleton, C. David  
APPLICANT: Nara, Peter  
APPLICANT: Shital, Mutsunori  
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES  
TITLE OF INVENTION: THAT ELICIT  
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND  
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/060,988A  
FILING DATE: 14-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/847,311  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/751,998  
FILING DATE: 29-AUG-1991  
APPLICATION NUMBER: 07/148,692  
FILING DATE: 26-JAN-1988

ATTORNEY/AGENT INFORMATION:  
NAME: Beattie, Ingrid A.  
REGISTRATION NUMBER: P-42,306  
REFERENCE/DOCKET NUMBER: 08830/022001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-060-988A-28

Query Match 83.8%; Score 171; DB 4; Length 39;  
Best Local Similarity 91.7%; Pred. No. 2.3e-17;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KQIINMDEVKAMYPISQIRIRHIGPGRAFT 36  
Db 1 KQIINMDEVKAMYPISQIRIRHIGPGRAFT 36

RESULT 8  
PCT-US94-05142-28  
Sequence 28, Application PC/TUS9405142  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT  
TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T  
NUMBER OF INVENTION: LYMPHOCYTES AGAINST HIV  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Birch, Stewart, Kolasch & Birch  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05142  
FILING DATE: 13-MAY-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/060,988  
FILING DATE: 14-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30330  
REFERENCE/DOCKET NUMBER: 1173-434P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..39  
OTHER INFORMATION: /label= peptide  
OTHER INFORMATION: /note= "pctus3-18MN peptide, see Table VI"

PCT-US94-05142-28

Query Match 83.8%; Score 171; DB 5; Length 39;  
Best Local Similarity 91.7%; Pred. No. 2,3e-17;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOIIMMOEVGKAMYAPISGQIRIRKRGPGRAFYT 36  
DB 1 KOIIMMOEVGKAMYAPISGQIRIRHIGPGRAFYT 36

## RESULT 9

US-08-015-770B-8

; Sequence 8, Application US/08015770B  
; Patent No. 5683695

## GENERAL INFORMATION:

; APPLICANT: Shen, De Fen  
; APPLICANT: Wang, Chang Yi  
; TITLE OF INVENTION: Production of recombinant proteins  
; TITLE OF INVENTION: containing multiple antigenic determinants linked by  
; TITLE OF INVENTION: flexible domains  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: United Biomedical, Inc.  
; STREET: 25 Davids Drive  
; CITY: Hauppauge  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11788

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/015,770B  
; FILING DATE: 10-FEB-1993  
; CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

; NAME: Wilson, M. Lisa  
; REGISTRATION NUMBER: 34,045  
; REFERENCE/DOCKET NUMBER: 2002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516)273-2828  
; TELEFAX: (516)273-1717  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 150 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-015-770B-8

Query Match 71.8%; Score 146.5; DB 1; Length 150;  
Best Local Similarity 68.9%; Pred. No. 2,9e-13;  
Matches 31; Conservative 1; Mismatches 4; Indels 9; Gaps 1;

QY 1 KOIIMMOEVGKAMYAPISGQIR-----RIORGPGRAFYT 36  
DB 4 KOIIMMOEVGKAMYAPISGQIRCPPPPDKPAHIGGRAFYT 48

## RESULT 10

US-08-455-625-24

; Sequence 24, Application US/08455625  
; Patent No. 5932218

## GENERAL INFORMATION:

; APPLICANT: Berzofsky, Jay A.  
; APPLICANT: Ahlers, Jeffrey D.  
; APPLICANT: Pendleton, C. D.  
; APPLICANT: Nara, Peter

APPLICANT: Shirai, Mutsunori

TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT

TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T

TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch &amp; Birch

STREET: P.O. Box 747

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,625

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/060,988

FILING DATE: 14-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30330

REFERENCE/DOCKET NUMBER: 1173-434P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-205-8000

TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..24

OTHER INFORMATION: /label= peptide

OTHER INFORMATION: /note= "pclus3 peptide"

US-08-455-625-24

Query Match 62.3%; Score 127; DB 2; Length 24;

Best Local Similarity 100.0%; Pred. No. 1,9e-11;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIIMMOEVGKAMYAPISGQIR 24  
DB 1 KOIIMMOEVGKAMYAPISGQIR 24

## RESULT 11

US-08-407-252-3

; Sequence 3, Application US/08407252  
; Patent No. 5939074

## GENERAL INFORMATION:

; APPLICANT: Berzofsky, Jay A.  
; TITLE OF INVENTION: Multideterminant Peptide Antigens that  
; TITLE OF INVENTION: Stimulate Helper T Lymphocyte Response to HIV in a Range  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: Two Embarcadero Center, 8th Fl.  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/407,252  
FILING DATE: 20-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/109,730  
FILING DATE: 19-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/751,998  
FILING DATE: 29-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/492,318  
FILING DATE: 28-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/148,692  
FILING DATE: 26-JAN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/222,684  
FILING DATE: 21-JUL-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: KING, JEFFREY J.  
REGISTRATION NUMBER: 38515  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 206-623-6793  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: HIV-1  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..25  
OTHER INFORMATION: /label= peptide  
OTHER INFORMATION: /note= "synthetic peptide fragment of HIV-1 gp160"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..16  
OTHER INFORMATION: /label= peptide  
OTHER INFORMATION: /note= "peptide hp-26 in table 2"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 5..19  
OTHER INFORMATION: /label= peptide  
OTHER INFORMATION: /note= "peptide hp-28 in table 2"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 10..24  
OTHER INFORMATION: /label= peptide  
OTHER INFORMATION: /note= "peptide hp-29 in table 2"  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: US 5,030,449  
FILING DATE: 21-JUL-1988  
PUBLICATION DATE: 09-JUL-1991  
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 20  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: US 07/148,692  
FILING DATE: 26-JAN-1988  
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 20  
US-08-407-252-3

Query Match 62.3%, Score 127, DB 2, Length 24;  
Best Local Similarity 100.0%, Pred. No. 1.9e-11;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KOIINMGEVGMKAYAPPSGQR 24  
|||||  
Db 1 KOIINMGEVGMKAYAPPSGQR 24

RESULT 12  
US-08-455-685-24  
Sequence 24, Application US/08455685  
Patent No 6214347  
GENERAL INFORMATION:  
APPLICANT: Beizofsky, Jay A.  
APPLICANT: Ahlers, Jeffrey D.  
APPLICANT: Pendleton, C. David  
APPLICANT: Nara, Peter  
APPLICANT: Shirai, Mutsunori  
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES THAT ELICIT  
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND  
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,685  
FILING DATE: 31-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/060,988  
FILING DATE: 14-MAY-1993  
APPLICATION NUMBER: 07/847,311  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/751,998  
FILING DATE: 29-AUG-1991  
APPLICATION NUMBER: 07/148,692  
FILING DATE: 26-JAN-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Beattie, Ingrid A.  
REGISTRATION NUMBER: P-42,306  
REFERENCE/DOCKET NUMBER: 08830/022003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-455-685-24

Query Match 62.3%, Score 127, DB 4, Length 24;  
Best Local Similarity 100.0%, Pred. No. 1.9e-11;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOIINMGEVGMKAYAPPSGQR 24  
|||||  
Db 1 KOIINMGEVGMKAYAPPSGQR 24

RESULT 13  
US-08-060-988A-24





Wed Jan 2 10:00:38 2002

us-09-508-552-2.rai

Page 8

Search completed: January 2, 2002, 09:56:51  
Job time: 21 sec

1 FILING DATE: 424  
 2 CLASSIFICATION: 424  
 3 PRIOR APPLICATION DATA:  
 4 APPLICATION NUMBER: 08\326,676  
 5 FILING DATE: 07-Jun-1995  
 6 APPLICATION NUMBER: 07\726,605  
 7 FILING DATE: 09-July-1991  
 8 APPLICATION NUMBER: 07\653,262  
 9 FILING DATE: 01-Mar-1991  
 10 APPLICATION NUMBER: 07\155,321  
 11 FILING DATE: 12-Feb-1988  
 12 ATTORNEY/AGENT INFORMATION:  
 13 NAME: Marcia C. H. Lin  
 14 REGISTRATION NUMBER: 29,323  
 15 REFERENCE/DOCKET NUMBER: 1151-4004 US  
 16 TELECOMMUNICATION INFORMATION:  
 17 TELEPHONE: 212-758-4800  
 18 TELEFAX: (212) 751-6849  
 19 TELE: 421792  
 20 INFORMATION FOR SEQ ID NO: 1:  
 21 SEQUENCE CHARACTERISTICS:  
 22 LENGTH: 28 amino acids  
 23 TYPE: Amino acid  
 24 STRANDEDNESS:  
 25 TOPOLOGY: unknown  
 26 MOLECULE TYPE: Peptide  
 27 HYPOTHEetical: No  
 28 ANTI-SENSE: No  
 29 FRAGMENT TYPE:  
 30 ORIGINAL SOURCE:  
 31 ORGANISM:  
 32 STRAIN:  
 33 INDIVIDUAL ISOLATE:  
 34 DEVELOPMENTAL STAGE:  
 35 HAPLOTYPE:  
 36 TISSUE TYPE:  
 37 CELL TYPE:  
 38 CELL LINE:  
 39 ORGNELLE:  
 40 IMMEDIATE SOURCE:  
 41 LIBRARY:  
 42 CLONE:  
 43 POSITION IN GENOME:  
 44 CHROMOSOME/SEGMENT:  
 45 MAP POSITION:  
 46 UNITS:  
 47 FEATURE:  
 48 NAME/KEY:  
 49 LOCATION:  
 50 IDENTIFICATION METHOD:  
 51 OTHER INFORMATION:  
 52 PUBLICATION INFORMATION:  
 53 AUTHORS:  
 54 TITLE:  
 55 JOURNAL:  
 56 VOLUME:  
 57 ISSUE:  
 58 PAGES:  
 59 DATE:  
 60 DOCUMENT NUMBER:  
 61 FILING DATE:  
 62 PUBLICATION DATE:  
 63 RELEVANT RESIDUES IN SEQ ID NO:  
 64 75-08-488-752-1





GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: January 2, 2002, 09:56:30 ; Search time 13.57 Seconds  
(without alignments)  
218.925 Million cell updates/sec

Title: US-09-508-552-2

Perfect score: 204  
Sequence: 1 KQIINMDEVGKAMYAPISGQIRIRGPGRAFTGK 39

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	62.3	851	2 S33985	env polyprotein -
2	127	62.3	856	1 VCLJH3	env polyprotein pr
3	123	60.3	506	2 A40218	envelop glycoprote
4	123	60.3	854	2 S13288	env protein - huma
5	123	60.3	856	1 VCLJVL	env polyprotein pr
6	123	60.3	859	1 VCLJMN	env polyprotein pr
7	123	60.3	861	1 VCLJLV	env polyprotein pr
8	122	59.8	290	2 S25940	env protein - huma
9	122	59.8	297	2 S60538	envelope polyprote
10	122	59.8	443	2 C41621	env polyprotein p
11	122	59.8	843	1 H44001	env polyprotein pr
12	122	59.8	847	2 T09448	envelope glycoprot
13	121	59.3	445	2 A41621	env polyprotein M
14	121	59.3	729	1 VCLJRX	env polyprotein pr
15	121	59.3	861	1 VCLJKB	env polyprotein pr
16	119	58.3	852	1 VCLJBR	env protein - huma
17	118	57.8	847	2 S13289	env polyprotein pr
18	118	57.8	855	1 VCLJAZ	envelope glycoprot
19	116	56.9	852	2 T12016	env polyprotein pr
20	116	56.9	856	1 VCLJ3W	env polyprotein pr
21	116	56.9	861	1 VCLJSC	env polyprotein pr
22	114	55.9	454	2 B41621	envelope polyprote
23	111	54.4	853	1 S54384	env polyprotein D
24	111	54.4	855	1 VCLJZK	env polyprotein pr
25	110	53.9	300	2 S60522	envelope polyprote
26	109	53.4	294	2 S60525	envelope polyprote
27	109	53.4	300	2 S60547	envelope polyprote
28	109	53.4	300	2 S60546	envelope polyprote
29	109	53.4	301	2 S60548	envelope polyprote

30	106	52.0	294	2 S60545	envelope polyprote
31	106	52.0	294	2 S60524	envelope polyprote
32	106	52.0	301	2 S60532	envelope polyprote
33	106	52.0	301	2 S60531	envelope polyprote
34	105	51.5	303	2 S60550	envelope polyprote
35	105	51.5	303	2 S60549	envelope polyprote
36	104	51.0	299	2 S60529	envelope polyprote
37	104	51.0	299	2 S60552	envelope polyprote
38	104	51.0	299	2 S60521	envelope polyprote
39	104	51.0	299	2 S60551	envelope polyprote
40	104	51.0	299	2 S60553	envelope polyprote
41	104	51.0	299	2 S60553	envelope polyprote
42	104	51.0	299	2 S60554	envelope polyprote
43	104	51.0	495	2 S31493	env polyprotein pr
44	104	51.0	846	1 VCLJND	env polyprotein pr
45	104	51.0	856	1 A44963	env polyprotein pr

## ALIGNMENTS

## RESULT 1

S33985  
env polyprotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1 HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S33985  
R:Carlini, F.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <CAR>  
A:Cross-references: EMBL:211530; NID:960192; PIDN:CAA77628.1; PID:960199  
C:Superfamily: type E retrovirus env polyprotein

## Query Match

Best local Similarity 62.3%; Score 127; DB 2; Length 851;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIINMDEVGKAMYAPISGQIR 24

DB 416 KQIINMDEVGKAMYAPISGQIR 439

## RESULT 2

VCLJH3  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH

N;Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

C:Accession: A03973

R:Ratner, L.; Haseltine, W.; Patarca, R.; Lyvak, K.J.; Starcich, B.; Josephs, S.F.; D  
nuberg, J.A.; Papas, T.S.; Chirgwin, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985

A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

A:Reference number: A93353; M0ID:85111123

A:Accession: A03973

A:Molecule type: DNA

A:Residues: 1-856 <RAT>

A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-511/Product: exterior membrane glycoprotein #status predicted <TM>

F:512-856/Product: transmembrane glycoprotein #status predicted <TM>

F:88-136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 62.3%; Score 127; DB 1; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIIMMOEVCAMYPISQIR 24  
 DB 421 KOIIMMOEVCAMYPISQIR 444

# RESULT 3

env polyprotein gp120 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 12-Apr-1995  
 C:Accession: A40218  
 R:Turner, S.; Tizard, R.; Demarins, J.; Peplinsky, R.B.; Zullo, J.; Schooley, R.; Fisher  
 Proc. Natl. Acad. Sci. U.S.A. 89, 1335-1339, 1992  
 A:Title: Resistance of primary isolates of human immunodeficiency virus type 1 to neutra  
 A:Reference number: A40218; MUID:92159044  
 A:Accession: A40218  
 A:Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-506 <TUR>  
 A:Experimental source: isolate P17  
 A:Note: sequence extracted from NCBI backbone (NCBI:82240)  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: glycoprotein

Query Match 60.3%; Score 123; DB 2; Length 506;  
 Best Local Similarity 95.8%; Pred. No. 4.3e-09;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOIIMMOEVCAMYPISQIR 24  
 DB 414 KOIIMMOEVCAMYPISQIR 437

# RESULT 4

env polyprotein - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
 C:Accession: S13288  
 R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A  
 Nature 348, 69-73, 1990  
 A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
 A:Reference number: S13288; MUID:91043044  
 A:Accession: S13288  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-854 <ORF>  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 60.3%; Score 123; DB 2; Length 854;  
 Best Local Similarity 95.8%; Pred. No. 7.4e-09;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOIIMMOEVCAMYPISQIR 24  
 DB 419 KOIIMMOEVCAMYPISQIR 442

# RESULT 5

env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

C:Accession: A03974  
 R:Mesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J  
 Nature 313, 450-458, 1985  
 A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr  
 A:Reference number: A93355; MUID:85111157  
 A:Accession: A03974  
 A:Molecule type: DNA  
 A:Residues: 1-856 <MUE>  
 A:Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559  
 C:Genetics:

A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
 F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
 F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,  
 F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status pre

Query Match 60.3%; Score 123; DB 1; Length 856;  
 Best Local Similarity 95.8%; Pred. No. 7.4e-09;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOIIMMOEVCAMYPISQIR 24  
 DB 421 KOIIMMOEVCAMYPISQIR 444

# RESULT 6

env polyprotein precursor - human immunodeficiency virus type 1 (isolate MN)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
 C:Accession: A28922  
 R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-  
 Virology 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; MUID:88219542  
 A:Accession: A28922  
 A:Molecule type: DNA  
 A:Residues: 1-859 <GUR>  
 C:Genetics:

A:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane pr  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-859/Product: env polyprotein #status predicted <EP>  
 F:87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,

Query Match 60.3%; Score 123; DB 1; Length 859;  
 Best Local Similarity 95.8%; Pred. No. 7.4e-09;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOIIMMOEVCAMYPISQIR 24  
 DB 424 KOIIMMOEVCAMYPISQIR 447

# RESULT 7

env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
 C:Accession: A03975  
 R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allizon, M.  
 Cell 40, 9-17, 1985  
 A:Title: Nucleotide sequence of the AIDS virus, LAV.

A:Reference number: A90866; MUID:85099333  
A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <MA1>  
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypotein  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-516/Product: exterior membrane glycoprotein #status predicted <TM>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F:88-136,141,146,161,165,191,202,246,267,281,294,300,306,337,344,361,391,397,402,411  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 60.3%; Score 123; DB 1; Length 861;  
Best Local Similarity 95.8%; Pred. No. 7.4e-09;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOIINMGEVGRKAMYAPPISQIR 24  
Db 426 KOIINMGEVGRKAMYAPPISQIR 449

RESULT 8  
S25940  
env protein - human immunodeficiency virus type 1 (fragment)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 22-Nov-1993 #sequence\_revision 30-Jan-1998 #text\_change 26-Aug-1999  
C:Accession: S25940  
R:Guo, H.G.; Chermann, J.C.; Waters, D.; Hall, L.; Louie, A.; Gallo, R.C.; Streicher, H.  
Nature 349, 745-746, 1991  
A:Title: Sequence analysis of original HIV-1.  
A:Reference number: S25937; MUID:91156044  
A:Accession: S25940  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-290 <GUO>  
A:Cross-references: EMBL:X57449; NID:g60208; PIDN:CAA0695.1; PID:g60209  
A:Experimental source: strain JBB  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1991  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: coat protein

Query Match 59.8%; Score 122; DB 2; Length 290;  
Best Local Similarity 95.8%; Pred. No. 3.3e-09;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOIINMGEVGRKAMYAPPISQIR 24  
Db 145 KOIINMGEVGRKAMYAPPISQIR 168

RESULT 9  
S60538  
env polyprotein gp41 - human immunodeficiency virus type 1 (isolate CI-22-3 and other  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate CI-22-3; isolate CI-22-6; isolate CI-22-10  
C:Date: 20-Jul-1996 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S60538; S60539; S60540  
R:Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;  
AIDS 8, 21-26, 1994  
A:Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote  
A:Reference number: S60521; MUID:94280700  
A:Accession: S60538  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-297 <JAN>  
A:Cross-references: EMBL:X72040; NID:g468655; PIDN:CAA50923.1; PID:g468656

A:Experimental source: isolate CI-22-3  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993  
A:Accession: S60539  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-297 <JAN>  
A:Cross-references: EMBL:X72041; NID:g468657; PIDN:CAA50924.1; PID:g468658  
A:Experimental source: isolate CI-22-6  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993  
A:Accession: S60540  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-297 <JAN>  
A:Cross-references: EMBL:X72042; NID:g468659; PIDN:CAA50925.1; PID:g468660  
A:Experimental source: isolate CI-22-10  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: AIDS; glycoprotein; immunodeficiency; polypotein

Query Match 59.8%; Score 122; DB 2; Length 297;  
Best Local Similarity 95.8%; Pred. No. 3.4e-09;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOIINMGEVGRKAMYAPPISQIR 24  
Db 148 KOIINMGEVGRKAMYAPPISQIR 171

RESULT 10  
C41621  
env polypotein P - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat polypotein  
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: C41621  
R:Bugner, H.; Welser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11336-11340, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A:Reference number: A41621; MUID:92107924  
A:Accession: C41621  
A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015  
A:Note: this virus was isolated from the mother's sexual partner  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypotein  
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:252-443/Product: coat protein gp41 (fragment) #status predicted <TM>  
F:442-443/Domain: transmembrane #status predicted <TM>  
F:9,23,36,46,76,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:

Query Match 59.8%; Score 122; DB 2; Length 443;  
Best Local Similarity 95.8%; Pred. No. 5.1e-09;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOIINMGEVGRKAMYAPPISQIR 24  
Db 161 KOIINMGEVGRKAMYAPPISQIR 184

RESULT 11  
H44001  
env polypotein precursor - human immunodeficiency virus type 1 (strain YU-2)  
N:Alternate names: coat polypotein  
N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Sep-1994  
C:Accession: H44001  
R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.  
J. Virol. 66, 6587-6600, 1992  
A:Title: Complete nucleotide sequence, genome organization, and biological properties of  
A:Reference number: M44001; MUID:93021387  
A:Accession: H44001  
A:Molecule type: DNA  
A:Residues: 1-843 <LTY>  
A:Cross-references: GB:M93258  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-79/Domain: signal sequence #status predicted <SIG>  
F:119-35/Region: hydrophobic  
F:330-489/Product: coat protein gp120 #status predicted <GP1>  
F:490-843/Product: coat protein gp41 #status predicted <GP2>  
F:499-515/Region: hydrophobic  
F:673-689/Region: hydrophobic  
F:738-755/Domain: transmembrane #status predicted <TMN>  
F:87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435

Query Match 59.8%; Score 122; DB 1; Length 843;  
Best Local Similarity 95.8%; Pred. No. 1e-08;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQIINMGOEVGKAMYAPPIRQIR 24  
DB 408 KQIINMGOEVGKAMYAPPIRQIR 431

RESULT 12  
T09448  
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRF1)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999  
C:Accession: T09448  
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,  
submitted to the EMBL Data Library, July 1996  
A:Reference number: Z16673  
A:Accession: T09448  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-847 <PAN>  
A:Cross-references: EMBL:U63632; NID:q1465777; PID:q1465781  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein

Query Match 59.8%; Score 122; DB 2; Length 847;  
Best Local Similarity 95.8%; Pred. No. 1e-08;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQIINMGOEVGKAMYAPPIRQIR 24  
DB 412 KQIINMGOEVGKAMYAPPIRQIR 435

RESULT 13  
A41621  
env polyprotein M - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat polyprotein  
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: A41621  
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A:Reference number: A41621; MUID:92107924  
A:Accession: A41621  
A:Molecule type: DNA  
A:Residues: 1-445 <BUR>  
A:Cross-references: GB:M77228; NID:9328627; PID:MAB03790.1; PID:9555013  
A:Note: this virus was isolated from the mother  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly  
F:1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F:426-445/Domain: transmembrane #status predicted <TMN>  
F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding s1

Query Match 59.3%; Score 121; DB 2; Length 445;  
Best Local Similarity 91.7%; Pred. No. 7.1e-09;  
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQIINMGOEVGKAMYAPPIRQIR 24  
DB 163 KQIINMGOEVGKAMYAPPIRQIR 186

RESULT 14  
VCLJRX  
env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)  
N:Alternate names: coat polyprotein  
N:Contains: coat protein gp120; coat protein gp32  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 01-Mar-1996  
C:Accession: B42995  
R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.  
Virology 189, 534-546, 1992  
A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncat  
A:Reference number: A42995; MUID:92351552  
A:Accession: B42995  
A:Molecule type: mRNA  
A:Residues: 1-729 <SHR>  
A:Cross-references: GB:S41266; GB:D01206  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-689/Domain: extracellular #status predicted <EXT>  
F:1-33/Domain: signal sequence #status predicted <SIG>  
F:17-33/Region: hydrophobic #status predicted  
F:34-517/Product: coat protein gp120 #status predicted <CP1>  
F:514-517/Region: cleavage processing #status predicted  
F:518-729/Product: coat protein gp32 #status predicted <CP2>  
F:518-534/Region: hydrophobic #status predicted  
F:690-711/Domain: transmembrane #status predicted <TMN>  
F:712-729/Domain: intracellular #status predicted <INT>  
F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,

Query Match 59.3%; Score 121; DB 1; Length 729;  
Best Local Similarity 91.7%; Pred. No. 1.2e-08;  
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQIINMGOEVGKAMYAPPIRQIR 24  
DB 422 KQIINMGOEVGKAMYAPPIRQIR 445

RESULT 15  
VCLJRX  
env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)  
N:Alternate names: coat polyprotein



N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 01-Mar-1996  
C:Accession: A42995  
R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.  
Virology 189, 534-546, 1992  
A:title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated  
A:Reference number: A42995; MOID:92351552  
A:Accession: A42995  
A:Molecule type: mRNA  
A:Residues: 1-861 <SH1>  
A:Cross-references: GB:S41266; GB:D01206  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-689/Domain: extracellular #status predicted <EXT>  
F:1-33/Domain: signal sequence #status predicted <SIG>  
F:17-33/Region: hydrophobic #status predicted  
F:34-517/Product: coat protein gp120 #status predicted <CP1>  
F:514-517/Region: cleavage processing #status predicted  
F:518-861/Product: coat protein gp41 #status predicted <CP2>  
F:518-534/Region: hydrophobic #status predicted  
F:680-711/Domain: transmembrane #status predicted <TM1>  
F:712-861/Domain: intracellular #status predicted <INT>  
F:756-772/Region: hydrophobic #status predicted  
F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 59.38; Score 121; DB 1; Length 861;  
Best Local Similarity 91.78; Pred. No. 1.4e-08;  
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOIYMMQEVGKAMYAPPISQIR 24  
|||||  
Db 422 KOIYMMQEVGKAMYAPPISQIR 445

Search completed: January 2, 2002, 09:57:42  
Job time: 72 sec



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OM protein - protein search, using sw model

Run on: January 2, 2002, 09:56:30 ; Search time 10.15 Seconds

(without alignments)  
140,880 Million cell updates/sec

Title: US-09-508-552-2

Perfect score: 204  
Sequence: 1 KOIMMOEVGKAMYAPISQIRRIORGPGRAPVTIGK 39

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	62.3	851	ENV_HV1B8	P04582 human immun
2	127	62.3	856	ENV_HV1B1	P03375 human immun
3	127	62.3	856	ENV_HV1I1	O70626 human immun
4	126	61.8	855	ENV_HV1OY	P20888 human immun
5	125	61.3	865	ENV_HV1RH	P04579 human immun
6	123	60.3	848	ENV_HV1LR	P20871 human immun
7	123	60.3	852	ENV_HV1S3	P19549 human immun
8	123	60.3	853	ENV_HV1K6	P19551 human immun
9	123	60.3	856	ENV_HV1H2	P04578 human immun
10	123	60.3	856	ENV_HV1H3	P04624 human immun
11	123	60.3	856	ENV_HV1M1	P05877 human immun
12	123	60.3	856	ENV_HV1PV	P03376 human immun
13	123	60.3	861	ENV_HV1BR	P03377 human immun
14	123	60.3	867	ENV_HV1J3	P12469 human immun
15	122	59.8	843	ENV_HV1Y2	P35961 human immun
16	121	59.3	861	ENV_HV1KB	P31819 human immun
17	119	58.3	855	ENV_HV1BN	P12468 human immun
18	118	57.8	855	ENV_HV1A2	P03378 human immun
19	116	56.9	847	ENV_HV1S1	P19550 human immun
20	116	56.9	847	ENV_HV1W2	P05880 human immun
21	116	56.9	856	ENV_HV1SC	P05878 human immun
22	116	56.9	856	ENV_HV1W1	P21872 human immun
23	111	54.4	853	ENV_HV1I2	P12467 human immun
24	111	54.4	855	ENV_HV1Z6	P04580 human immun
25	106	52.0	863	ENV_HV1Z8	P05882 human immun
26	104	51.0	846	ENV_HV1MD	P18789 human immun
27	104	51.0	856	ENV_HV1ZB	P05881 human immun
28	104	51.0	859	ENV_HV1MA	P04583 human immun
29	93	45.6	868	ENV_HV1C4	P05879 human immun
30	92	45.1	460	ENV_HV1Z3	P12491 human immun
31	79	38.7	712	ENV_HV2S2	P23536 human immun
32	79	38.7	859	ENV_HV2ST	P20872 human immun
33	76	37.3	851	ENV_HV2G1	P18040 human immun

34	76	37.3	854	1	ENV_STVCL	p17281 chimpanzee
35	76	37.3	860	1	ENV_HV2BE	p18094 human immun
36	73	35.8	856	1	ENV_HV2N2	P05883 human immun
37	73	35.8	858	1	ENV_HV2RO	P04577 human immun
38	73	35.8	859	1	ENV_HV2CA	P24105 human immun
39	73	35.8	859	1	ENV_HV2D2	P15831 human immun
40	72	35.3	846	1	ENV_HV2SB	P12449 human immun
41	71	34.8	880	1	ENV_STVW2	P08810 simian immu
42	71	34.8	880	1	ENV_STVWL	P11267 simian immu
43	71	34.8	881	1	ENV_STVWK	P05884 simian immu
44	71	34.8	882	1	ENV_STVWL	P05885 simian immu
45	71	34.8	885	1	ENV_STV54	P12492 simian immu

## ALIGNMENTS

RESULT	ID	ENV_HV1B8	STANDARD	PRT	851 AA.
AC	P04582				
DT	13-AUG-1987 (Rel. 05, Created)				
DT	13-AUG-1987 (Rel. 05, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)]				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).				
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11684				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8511123; PubMed=2578615				
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Pappas T.S., Graybe J., Chang N.T., Gallo R.C., Launderberger J.A., Wons-Staal F.;				
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III."				
RT	Nature 313:277-284(1985).				
RL	-----				
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CC	-----				
DR	EMBL; K02011; AAA44661.1; -				
DR	HIV; K02011; ENV58B8.				
DR	GlycoSuiteDB; P04582; -				
DR	InterPro; IPR000328; Env.GP41.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120; 1.				
DR	Pfam; PF00517; GP41; 1.				
KW	Aids; Coat protein; Glycoprotein; Glycoprotein; Transmembrane; signal.				
FT	SIGNAL	1	30		
FT	CHAIN	31	506		EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	851		TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74		BY SIMILARITY.
FT	DISULFID	119	205		BY SIMILARITY.
FT	DISULFID	126	196		BY SIMILARITY.
FT	DISULFID	131	157		BY SIMILARITY.
FT	DISULFID	218	247		BY SIMILARITY.
FT	DISULFID	228	239		BY SIMILARITY.
FT	DISULFID	228	239		BY SIMILARITY.
FT	DISULFID	296	331		BY SIMILARITY.
FT	DISULFID	378	440		BY SIMILARITY.
FT	DISULFID	385	413		BY SIMILARITY.
FT	CARBOHYD	88	88		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	141	141		N-LINKED (GLCNAC. . .) (POTENTIAL).

```
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;
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Query Match 62.3%; Score 127; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 KOIIMMOEVGKAMYAPISGOIR 24
    |||||
Db 416 KOIIMMOEVGKAMYAPISGOIR 439
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```
RESULT 2
ENV_HV1B1 STANDARD; PRT; 856 AA.
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AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
CN ENV.
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11678;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; PubMed=2578615.
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Katalinski J.A., Whitehorn E.A.,
RA Baumeshter K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).
RN [2]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
RT potential glycosylation sites of the type 1 recombinant human
RT immunodeficiency virus envelope glycoprotein (gp120) expressed in
RT Chinese hamster ovary cells";
RL J. Biol. Chem. 265:10373-10382(1990).
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DR EMBL: M15654; AAA44205.1; -.
DR PIR: A03973; VCLJH3.
DR HTV; M15654; ENV$BH102.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
```

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FT SIGNAL 1 30
FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 131 247
FT DISULFID 218 228
FT DISULFID 228 239
FT DISULFID 228 331
FT DISULFID 296 378
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97224 MW; 0BPF1A18931BB27 CRC64;
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Query Match 62.3%; Score 127; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 KOIIMMOEVGKAMYAPISGOIR 24
    |||||
Db 421 KOIIMMOEVGKAMYAPISGOIR 444
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RESULT 3
ENV_HV1LW
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ID	ENV_HVILW	STANDARD:	PRT:	856 AA.
AC	G070626;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].			
CN	ENV.			
OS	Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirinae.			
OX	NCBI_TaxId=82834;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95127297; PubMed=7826699;			
RA	Reitz M.S., Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M., Shaw G.M., Kong L.I., Weiss S.H., Walters D., Gallo R.C., Blattner W.;			
RT	"Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HTLV type IIIB)." ;			
RL	AIDS Res. Hum. Retroviruses 10:1143-1155(1994).			
CC	-----			
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CC	or send an email to license@isb.ch).			
CC	-----			
DR	EMBL: U12055; AAA76690.1; -.			
DR	GlycoSuiteDB: G070626; -.			
DR	InterPro: IPR000328; Env_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	30	
FT	CHAIN	31	511	
FT	CHAIN	512	856	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	119	205	BY SIMILARITY.
FT	DISULFID	126	196	BY SIMILARITY.
FT	DISULFID	131	157	BY SIMILARITY.
FT	DISULFID	218	247	BY SIMILARITY.
FT	DISULFID	228	239	BY SIMILARITY.
FT	DISULFID	296	331	BY SIMILARITY.
FT	DISULFID	378	445	BY SIMILARITY.
FT	DISULFID	385	418	BY SIMILARITY.
FT	CARBOHYD	88	88	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	156	156	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	160	160	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	197	197	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	230	230	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	234	234	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	241	241	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	262	262	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	276	276	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	289	289	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	301	301	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	339	339	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	356	356	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	366	366	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	392	392	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	397	397	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	406	406	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	448	448	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	463	463	N-LINKED (GLCNAC . . ) (POTENTIAL).
FT	CARBOHYD	611	611	N-LINKED (GLCNAC . . ) (POTENTIAL).

FT	CARBOHYD	616	616	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	637	637	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	674	674	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	750	750	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	816	816	N-LINKED (GLCNAC. . . ) (POTENTIAL).
SO	SEQUENCE	856 AA;	96938 MW;	0C24I332CF76687 CXC64;
Query Match		62.3%;	Score 127;	DB 1;
Best Local Similarity		100.0%;	Pred. No. 3.3e-10;	
Matches 24;		Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1 KOIIMMOEVGKAMYAPISGOIR 24			
DB	421 KOIIMMOEVGKAMYAPISGOIR 444			
RESULT	4	ENV_HV10Y	STANDARD;	PRT; 855 AA.
ID	ENV_HV10Y			
AC	P20888;			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].			
OS	ENV.			
OS	Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).			
CC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11699;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90148544; PubMed=2559749;			
RA	Huet T., Dazza M.C., Brun-Yezinet F., Roelants G.E., Mah-Hobson S.;			
RT	"A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";			
RL	AIDS 3:707-715(1989).			
CC	-1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.			
CC	-----			
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CC	-----			
DR	EMBL; M26727; AAA83397.1; -.			
DR	HIV; M26727; ENVSOYT.			
DR	InterPro: IPR000328; ENV_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	ADIS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.			
KW	SIGNAL.	1	29	
FT	CHAIN	30	509	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	510	855	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	210	BY SIMILARITY.
FT	DISULFID	125	201	BY SIMILARITY.
FT	DISULFID	130	162	BY SIMILARITY.
FT	DISULFID	223	252	BY SIMILARITY.
FT	DISULFID	233	244	BY SIMILARITY.
FT	DISULFID	301	335	BY SIMILARITY.
FT	DISULFID	381	442	BY SIMILARITY.
FT	DISULFID	388	415	BY SIMILARITY.
FT	CARBOHYD	87		N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	145	145	N-LINKED (GLCNAC. . . ) (POTENTIAL).

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      FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).
      SQ SEQUENCE 835 AA; 97476 MW; 9CF82A607ADD62DA CRC64;

Query Match 61.8%; Score 126; DB 1; Length 855;
Best Local Similarity 95.8%; Pred. No. 4.6e-10;
Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOEYKAMVAPISQIR 24
Db 418 KOIINMOEYKAMVAPISQIR 441
|||||
RESULT 5
ENV_HV1RH STANDARD; PRT; 865 AA.
AC P04579;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
ON NCB1_Taxid=11701;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
RT "Identification and characterization of conserved and variable
RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of
RT AIDS.";
RL Cell 45:637-648 (1986).
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CC or send an email to license@isb-sib.ch).
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CC EMBL: M17451; AAA45057.1; .
CC HIV: M17451; ENVSRF.
CC Interpro: IPR000328; Env-GP41.
CC Interpro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC DR Pfam: PF00517; GP41; 1.
CC KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;

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```

      KW Signal. 1 29
      FT SIGNAL 30 519 EXTERIOR MEMBRANE GLYCOPROTEIN.
      FT CHAIN 520 865 TRANSMEMBRANE GLYCOPROTEIN.
      FT DISULFID 53 73 BY SIMILARITY.
      FT DISULFID 118 218 BY SIMILARITY.
      FT DISULFID 125 209 BY SIMILARITY.
      FT DISULFID 130 157 BY SIMILARITY.
      FT DISULFID 231 260 BY SIMILARITY.
      FT DISULFID 241 252 BY SIMILARITY.
      FT DISULFID 309 343 BY SIMILARITY.
      FT DISULFID 389 452 BY SIMILARITY.
      FT DISULFID 396 425 BY SIMILARITY.
      FT CARBOHYD 129 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 139 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 646 646 N-LINKED (GLCNAC. . .) (POTENTIAL).
      FT CARBOHYD 825 825 N-LINKED (GLCNAC. . .) (POTENTIAL).
      SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCAC CRC64;

Query Match 61.3%; Score 125; DB 1; Length 865;
Best Local Similarity 77.4%; Pred. No. 6.5e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 KOIINMOEYKAMVAPISQIRIORGP 31
Db 428 KOIINMOEYKAMVAPISQIRIORGP 458
|||||
RESULT 6
ENV_HV1JR STANDARD; PRT; 848 AA.
AC P20871;
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (JRCF isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
ON NCB1_Taxid=11688;
RN [1]
RP SEQUENCE FROM N.A.

```

Query Match	Best Local Similarity	Score 123:	DB 1:	Length 848:
Matches 23:	Conservative 0:	Mismatches 1:	Indels 0:	Gaps 0:
1 KOIINMNOEVGKAMYPISGQIR 24	95.8%	60.3%	123	848
413 KOIINMNOEVGKAMYPISGQIR 436	95.8%	60.3%	123	848

ID	ENV_HV1S3	STANDARD:	PRT;	852 AA.
AC	P19549;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentiviruses.			
OX	NCBI_TaxID=11690;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90317906; PubMed=2370688;			
RA	York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;			
RT	"Human immunodeficiency virus type 1 cellular host range,			
RT	replication, and cytopathicity are linked to the envelope region of			
RT	the viral genome.";			
RL	J. Virol. 64:4016-4020(1990).			
CC	-----			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL, M38427; AAA45067.1; -.			
DR	HIV; M38427; ENVSEF33.			
DR	InterPro: IPR000328; ENV_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KM	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;			
KM	Signal.			
FT	SIGNAL	1	31	BY SIMILARITY.
FT	CHAIN	32	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	852	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	206	BY SIMILARITY.
FT	DISULFID	125	197	BY SIMILARITY.
FT	DISULFID	130	156	BY SIMILARITY.
FT	DISULFID	219	248	BY SIMILARITY.
FT	DISULFID	229	240	BY SIMILARITY.
FT	DISULFID	297	331	BY SIMILARITY.
FT	DISULFID	377	439	BY SIMILARITY.
FT	DISULFID	384	412	BY SIMILARITY.
FT	CARBOHYD	87		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	129		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	136		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	141		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	142		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	145		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	159		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	189		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	198		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	242		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	263		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	277		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	290		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	296		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	332		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	339		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	355		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	385		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	391		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	397		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	401		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	405		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	442		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	457		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	607		N-LINKED (GLCNAC. . .)

FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 852 AA: 96663 MW: EE7BBF8D23C9910D CRC64;

Query Match 60.3%; Score 123; DB 1; Length 852;  
 Best Local Similarity 95.8%; Pred. No. 1.2e-09;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOIIMMOEYKAMYAPPISQIR 24  
 DB 415 KOIIMMOEYKAMYAPPISQIR 438

RESULT 8  
 ENV\_HV1MF STANDARD: PRT: 853 AA.  
 ID ENV\_HV1MF  
 AC P19551;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11704;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90317877; PubMed=1695254;  
 RA Stevenson M., Hagerty S., Lamouca C., Mann A.M., Meier C.,  
 RA Wasjak A.;  
 RT "Cloning and characterization of human immunodeficiency virus type 1  
 RT variants diminished in the ability to induce syncytium-independent  
 RT cytolysis.";  
 RL J. Virol. 64:3792-3803(1990).

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DR EMBL: M33943; AAA44850.1; -;  
 DR HIV: M33943; ENVSMFA.  
 DR InterPro: IPR000328; ENV\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 510 853 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 54 74 BY SIMILARITY.  
 FT DISULFID 119 203 BY SIMILARITY.  
 FT DISULFID 126 194 BY SIMILARITY.  
 FT DISULFID 131 157 BY SIMILARITY.  
 FT DISULFID 131 157 BY SIMILARITY.  
 FT DISULFID 216 245 BY SIMILARITY.  
 FT DISULFID 226 237 BY SIMILARITY.  
 FT DISULFID 294 329 BY SIMILARITY.  
 FT DISULFID 376 443 BY SIMILARITY.  
 FT DISULFID 383 416 BY SIMILARITY.  
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 853 AA: 96912 MW: 3377B993B6F22ABA CRC64;

Query Match 60.3%; Score 123; DB 1; Length 853;  
 Best Local Similarity 95.8%; Pred. No. 1.2e-09;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOIIMMOEYKAMYAPPISQIR 24  
 DB 419 KOIIMMOEYKAMYAPPISQIR 442

RESULT 9  
 ENV\_HV1H2 STANDARD: PRT: 856 AA.  
 ID ENV\_HV1H2  
 AC P04578; 009779;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11706;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8729196; PubMed=3040055;  
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,  
 RA Gallo R.C., Wong-Staal F.;  
 RT "Complete nucleotide sequences of functional clones of the AIDS  
 RT virus.";  
 RL AIDS Res. Hum. Retroviruses 3:57-69(1987).

REVISIONS.  
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,  
 RA Gallo R.C., Wong-Staal F.;  
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.

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DR EMBL: K03455; AAB50262.1; -;  
 DR EMBL: AF038399; AAB99976.1; -;  
 DR EMBL: AF038319; AAC82596.1; -;



[illegible][illegible]

PT	SIGNAL	1	29	EXTERIOR MEMBRANE GLYCOPROTEIN.
PT	CHAIN	30	513	TRANSMEMBRANE GLYCOPROTEIN.
PT	CHAIN	514	856	
PT	DISULFID	53	73	BY SIMILARITY.
PT	DISULFID	118	210	BY SIMILARITY.
PT	DISULFID	125	201	BY SIMILARITY.
PT	DISULFID	130	162	BY SIMILARITY.
PT	DISULFID	223	252	BY SIMILARITY.
PT	DISULFID	233	244	BY SIMILARITY.
PT	DISULFID	301	335	BY SIMILARITY.
PT	DISULFID	381	445	BY SIMILARITY.
PT	DISULFID	388	418	BY SIMILARITY.
PT	CARBOHYD	87	87	N-LINKED (GLCNAC. . . ) (POTENTIAL).
PT	CARBOHYD	129	129	N-LINKED (GLCNAC. . . ) (POTENTIAL).
PT	CARBOHYD	135	135	N-LINKED (GLCNAC. . . ) (POTENTIAL).
PT	CARBOHYD	140	140	N-LINKED (GLCNAC. . . ) (POTENTIAL).
PT	CARBOHYD	141	141	N-LINKED (GLCNAC. . . ) (POTENTIAL).
PT	CARBOHYD	146	146	N-LINKED (GLCNAC. . . ) (POTENTIAL).
PT	CARBOHYD	161	161	N-LINKED (GLCNAC. . . ) (POTENTIAL).
PT	CARBOHYD	165	165	N-LINKED (GLCNAC. . . ) (POTENTIAL).
PT	CARBOHYD	191	191	N-LINKED (GLCNAC. . . ) (POTENTIAL).
PT	CARBOHYD	202	202	N-LINKED (GLCNAC. . . ) (POTENTIAL).
PT	CARBOHYD	246	246	N-LINKED (GLCNAC. . . ) (POTENTIAL).
PT	CARBOHYD	267	267	N-LINKED (GLCNAC. . . ) (POTENTIAL).
PT	CARBOHYD	281	281	N-LINKED (GLCNAC. . . ) (POTENTIAL).

Accession	Protein Name	Length (aa)	Source
DR EMBL, X02083; AAB59873.1; -	EMBL, X01762; CAA25903.1; ALT_SEQ.	30	EXTERIOR MEMBRANE GLYCOPROTEIN.
DR PIR; A03974; VCLJVL.	HIV; X02083; ENVSPV22.	51	TRANSMEMBRANE GLYCOPROTEIN
DR InterPro: IPR000328; Env_Gp41.	InterPro: IPR000777; Gp120.	856	TRANSMEMBRANE GLYCOPROTEIN
DR InterPro: IPR000777; Gp120.	Pfam: PF00516; Gp120; 1.	512	TRANSMEMBRANE GLYCOPROTEIN
DR Pfam: PF00517; Gp41; 1.	AIDS: Coat protein; Polypotein; Glycoprotein; Transmembrane; Signal.	30	TRANSMEMBRANE GLYCOPROTEIN.
KW	Signal.	1	TRANSMEMBRANE GLYCOPROTEIN.
KM	Signal.	30	TRANSMEMBRANE GLYCOPROTEIN.
FT	SIGNAL	1	TRANSMEMBRANE GLYCOPROTEIN.
FT CHAIN	31	51	TRANSMEMBRANE GLYCOPROTEIN.
FT CHAIN	512	856	TRANSMEMBRANE GLYCOPROTEIN

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FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97339 MW; 5FCD81DC3C120983 CRC64;
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Query Match 60.3%; Score 123; DB 1; Length 856;
Best Local Similarity 95.8%; Pred. No. 1.2e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 KOIINMOEYKAMVAPISGOIR 24
Db 421 KOIINMOEYKAMVAPISGOIR 444
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RESULT 13
ENV_HV1BR STANDARD; PRT: 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8509333; PubMed=2981635;
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Allizon M.;
RA "Nucleotide sequence of the AIDS virus, LAV.";
RA Cell 40:9-17(1985).
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CC EMBL: K02013; AAB59751.1; -
CC EMBL: A04321; CA00352.1; -
CC PIR: A03975; VCLIVJ.
CC HTV; K02013; ENVSRU.
CC InterPro: IPR000328; Env_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC Pfam: PF00517; GP41; 1.
CC AIDS; Coat protein; polypeptide; glycoprotein; Transmembrane;
CC signal.
FT SIGNAL. 1 30
FT CHAIN 31 516
FT CHAIN 517 861
FT DISULFID 54 74
FT DISULFID 119 210
FT DISULFID 126 201
FT DISULFID 131 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 336
FT DISULFID 383 450
FT DISULFID 390 423
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 146 146
FT CARBOHYD 161 161
FT CARBOHYD 165 165
FT CARBOHYD 191 191
FT CARBOHYD 202 202
FT CARBOHYD 235 235
FT CARBOHYD 239 239
FT CARBOHYD 246 246
FT CARBOHYD 267 267
FT CARBOHYD 281 281
FT CARBOHYD 294 294
FT CARBOHYD 300 300
FT CARBOHYD 306 306
FT CARBOHYD 337 337
FT CARBOHYD 344 344
FT CARBOHYD 361 361
FT CARBOHYD 391 391
FT CARBOHYD 397 397
FT CARBOHYD 402 402
FT CARBOHYD 411 411
FT CARBOHYD 453 453
FT CARBOHYD 468 468
FT CARBOHYD 616 616
FT CARBOHYD 621 621
FT CARBOHYD 630 630
FT CARBOHYD 642 642
FT CARBOHYD 679 679
FT CARBOHYD 755 755
FT CARBOHYD 821 821
SQ SEQUENCE 861 AA; 97487 MW; 04DE2B4D4E4F63A CRC64;
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Query Match 60.3%; Score 123; DB 1; Length 861;
Best Local Similarity 95.8%; Pred. No. 1.2e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 KOIINMOEYKAMVAPISGOIR 24
Db 426 KOIINMOEYKAMVAPISGOIR 449
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RESULT 14
ENV_HV1J3 STANDARD: PRT: 867 AA.
ID ENV_HV1J3
PI2489:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV-1) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11694;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352108; PubMed=2669897;
RA Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
RT "Nucleotide sequences of gag and env genes of a Japanese isolate of
RT HIV-1 and their expression in bacteria."
RL AIDS Res. Hum. Retroviruses 5:411-419(1989).
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CC or send an email to license@isb-sib.ch).
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DR EMBL: M21138; AAB03526.1; -.
DR HIV: M21138; ENV5JH3.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 517 867 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73
FT DISULFID 118 217 BY SIMILARITY.
FT DISULFID 125 208 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 342 BY SIMILARITY.
FT DISULFID 388 457 BY SIMILARITY.
FT DISULFID 395 430 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 867 AA; 98399 MW; 5F2310146B8E8680 CRC64;

Query Match Score 123; DB 1; Length 867;
Best Local Similarity 95.8%; Pred. No. 1.3e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KOIINMOEYKAMYAPPIESQIR 24
Db 433 KOIINMOEYKAMYAPPIESQIR 456

RESULT 15
ENV_HV1Y2 STANDARD: PRT: 843 AA.
ID ENV_HV1Y2
AC P35961;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV-2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93021387; PubMed=1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
RA Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological
RT properties of human immunodeficiency virus type 1 in vivo: evidence
RT for limited defectiveness and complementation."
RL J. Virol. 66:6587-6600(1992).
-----
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DR EMBL: M93258; -. NOT_ANNOTATED_CDS.
DR PIR: H44001; H44001.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 489 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 490 843 TRANSMEMBRANE GLYCOPROTEIN.
FT CARBOHYD 738 755 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 738 755 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 118 201 BY SIMILARITY.
FT CARBOHYD 125 192 BY SIMILARITY.
FT CARBOHYD 130 155 BY SIMILARITY.
FT CARBOHYD 143 143 BY SIMILARITY.
FT CARBOHYD 214 243 BY SIMILARITY.
FT CARBOHYD 224 235 BY SIMILARITY.
FT CARBOHYD 292 326 BY SIMILARITY.
FT CARBOHYD 373 432 BY SIMILARITY.
FT CARBOHYD 380 405 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 598 598 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 803 803 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 843 AA; 95648 MW; C69DFD971C918B71 CRC64;
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Query Match 59.8%; Score 122; DB 1; Length 843;
Best Local Similarity 95.8%; Pred. No. 1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 KQIINMGEVKGAMYAPPISQIR 24
    |||||
Db 408 KQIINMGEVKGAMYAPPISQIR 431
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Search completed: January 2, 2002, 09:57:58  
Job time: 88 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 2, 2002, 09:56:30 ; Search time 22.85 Seconds  
(Without alignments)  
249.655 Million cell updates/sec

Title: US-09-508-552-2

Perfect score: 204  
Sequence: 1 KOIIMWQEVGKAMYAPISQIRRIQSGRAFTYIGK 39

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_17:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	129	63.2	203	12	Q9QE99 human immun
2	129	63.2	203	12	Q9J4T6 human immun
3	128	62.7	263	12	Q9WD03 human immun
4	128	62.7	396	12	O11498 human immun
5	127	62.3	68	12	Q97748 human immun
6	127	62.3	84	12	Q9QFG0 human immun
7	127	62.3	103	12	Q78883 human immun
8	127	62.3	106	12	Q78887 human immun
9	127	62.3	158	12	Q73109 human immun
10	127	62.3	158	12	Q73110 human immun
11	127	62.3	158	12	Q73111 human immun
12	127	62.3	158	12	Q73112 human immun
13	127	62.3	158	12	Q73113 human immun
14	127	62.3	158	12	Q73114 human immun
15	127	62.3	160	12	Q73107 human immun
16	127	62.3	160	12	Q73108 human immun
17	127	62.3	178	12	Q70611 human immun
18	127	62.3	183	12	Q70614 human immun
19	127	62.3	183	12	Q70609 human immun

20	127	62.3	183	12	Q70616 human immun
21	127	62.3	183	12	Q70617 human immun
22	127	62.3	183	12	Q70621 human immun
23	127	62.3	199	12	Q9JDM8 human immun
24	127	62.3	199	12	Q9JDM4 human immun
25	127	62.3	199	12	Q9JDM0 human immun
26	127	62.3	199	12	Q9JDM8 human immun
27	127	62.3	199	12	Q9JDM7 human immun
28	127	62.3	199	12	Q9JDM4 human immun
29	127	62.3	199	12	Q9JDM2 human immun
30	127	62.3	199	12	Q9JDM1 human immun
31	127	62.3	199	12	Q9JDM6 human immun
32	127	62.3	199	12	Q9JDM5 human immun
33	127	62.3	199	12	Q9JDM9 human immun
34	127	62.3	199	12	Q9JDM1 human immun
35	127	62.3	200	12	Q9JDM6 human immun
36	127	62.3	200	12	Q9JDM5 human immun
37	127	62.3	200	12	Q9JDM3 human immun
38	127	62.3	200	12	Q9JDM9 human immun
39	127	62.3	202	12	Q9JDM5 human immun
40	127	62.3	202	12	Q9JDM5 human immun
41	127	62.3	202	12	Q9JDM4 human immun
42	127	62.3	202	12	Q9JDM3 human immun
43	127	62.3	202	12	Q9JDM0 human immun
44	127	62.3	202	12	Q9JDM6 human immun
45	127	62.3	202	12	Q9JDM5 human immun

## ALIGNMENTS

RESULT 1  
Q9QE99 PRELIMINARY: PRT: 203 AA.

AC Q9QE99: 01-MAY-2000 (TRENBLREL. 13, Created)  
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)  
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
CN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Liu S.-L., Mulvania T., Rodrigo A.G., Kosloff B., He X., Shriner D., Schacker T., Shea T., Corey L., Mullins J.L.;  
RT "Emergence and Competitive Selection for Human Immunodeficiency Virus RT Type-1 Chimeras in Vivo."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF185336; AAF06409.1; -  
DR InterPro: IPR00777; GP120; 1.  
DR Pfam: PF00516; GP120; 1.  
KW Envelope protein.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 203 AA; 22702 MW; 7BC57648B5AAN32A CRC64;

Query Match 63.2%; Score 129; DB 12; Length 203;  
Best Local Similarity 96.0%; Pred. No. 6,2e-10;  
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIIMWQEVGKAMYAPISQIR 25  
Db 147 KOIIMWQEVGKAMYAPISGIR 171

RESULT 2  
ID Q9J4T6 PRELIMINARY: PRT: 298 AA.  
AC Q9J4T6: 01-OCT-2000 (TRENBLREL. 15, Created)  
DT 01-OCT-2000 (TRENBLREL. 15, Created)

01-OCF-2000 (Tremblrel. 15, last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=98MX.MC06;  
RA Rivera-Morales L.G., Novitsky V.A., Vannberg F., Trujillo J.R.,  
RT Tamez-Guerra R., Rodriguez-Padilla C., Essex M.,  
RL "HIV-1 subtype B is a predominant AIDS virus in Mexico."  
DR Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF200860; AAF27370.1; -  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
FT NON\_TER 1 298  
SQ SEQUENCE 298 AA; 33177 MW; D36E9011072499AA CRC64;

Query Match 63.2%; Score 129; DB 12; Length 298;  
Best Local Similarity 83.9%; Pred. No. 9.6e-10;  
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KOIINMOEVGKAMYAPISGQIRRTQSGPG 31  
Db 210 KOIINMOEVGKAMYAPISGQIRCSNITG 240

RESULT 3  
ID O9WDU3 PRELIMINARY; PRT; 263 AA.  
AC O9WDU3;  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D-DI-02;  
RA MEDLINE=9214314; PubMed=10196271;  
RA Bagarrelli P., Mazza F., Menzo S., Montironi M., Butini L.,  
RT Clementi M.;  
RT "Host-specific modulation of the selective constraints driving human  
RT immunodeficiency virus type 1 env gene evolution.";  
RL J. Virol. 73:3764-3777(1999).  
DR EMBL: AF105560; AAD27170.1; -  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KM Envelope protein.  
FT NON\_TER 1 263  
SQ SEQUENCE 263 AA; 29437 MW; 4A4D5C3626BE6895 CRC64;

Query Match 62.7%; Score 128; DB 12; Length 263;  
Best Local Similarity 96.0%; Pred. No. 1.1e-09;  
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOEVGKAMYAPISGQIR 25  
Db 163 KOIINMOEVGKAMYAPISGQIR 187

RESULT 4  
O11498 PRELIMINARY; PRT; 396 AA.

AC O11498;  
DT 01-JUL-1997 (Tremblrel. 04, Created)  
DT 01-JUL-1997 (Tremblrel. 04, last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Balotta C., Riva C., Violin M., Colombo C., Galli M., Moroni M.;  
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U95401; AAB52747.1; -  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KM Envelope protein.  
FT NON\_TER 1 396  
SQ SEQUENCE 396 AA; 44103 MW; 457EC5D0CA1A9E54 CRC64;

Query Match 62.7%; Score 128; DB 12; Length 396;  
Best Local Similarity 68.4%; Pred. No. 1.8e-09;  
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

OY 1 KOIINMOEVGKAMYAPISGQIRRTQSGPRAVITG 38  
Db 293 KOIINMOEVGKAMYAPISGQIRCSNITGLILTRVG 330

RESULT 5  
ID O97748 PRELIMINARY; PRT; 68 AA.  
AC O97748;  
DT 01-FEB-1997 (Tremblrel. 02, Created)  
DT 01-FEB-1997 (Tremblrel. 02, last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=92092169; PubMed=1684385;  
RA Pang S., Vinters H.V., Akashi T., O'Brien W.A., Chen T.S.;  
RT "HIV-1 env sequence variation in brain tissue of patients with AIDS-  
RT related neurologic disease.";  
RT J. Acquir. Immune Defic. Syndr. 4:1082-1092(1991).  
DR EMBL: M74988; AAB08908.1; -  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KM Envelope protein.  
FT NON\_TER 1 68  
SQ SEQUENCE 68 AA; 7662 MW; F5FBDADE121F7D19 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 68;  
Best Local Similarity 100.0%; Pred. No. 3.4e-10;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOEVGKAMYAPISGQIR 24  
Db 37 KOIINMOEVGKAMYAPISGQIR 60

RESULT 6  
O90FG0 PRELIMINARY; PRT; 84 AA.  
AC O90FG0;  
DT 01-MAY-2000 (Tremblrel. 13, Created)



DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LF33;  
RA MEDLINE=99412391; PubMed=10482626;  
RA Morris A., Marsden M., Halcrow K., Hughes E.S., Brettle R.P.,  
RA Bell J.E., Simmonds P.;  
RT "Mosaic structure of the human immunodeficiency virus type 1 genome  
RT infecting lymphoid cells and the brain: evidence for frequent in vivo  
RT recombination events in the evolution of regional populations.";  
RL J. Virol. 73:8720-8731(1999).  
DR EMBL: AF175038; AAF00384.1; -  
DR InterPro: IPR000777; GP120.1.  
DR Pfam: PF00516; GP120; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT SEQUENCE 84 AA: 9369 MW: 789D75FE6FFDBC11 CRC64;  
SQ

Query Match 62.3%; Score 127; DB 12; Length 84;  
Best Local Similarity 96.0%; Pred. No. 4.3e-10;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOIINMOEYKAMYAPPISQIR 25  
Db 30 KOIINMOEYKAMYAPPISQIR 54

RESULT 7  
078883 PRELIMINARY; PRT; 103 AA.  
AC 078883;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE ENVELOPE POLYPROTEIN (FRAGMENT).  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=5990;  
RA Ou C.Y., Kalish M.;  
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.  
DR EMBL: L07160; AAB06860.1; -  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW Polypeptide; Envelope protein.  
FT NON\_TER 1  
FT SEQUENCE 103 AA: 11179 MW: 2FD01547FAE76D51 CRC64;  
SQ

Query Match 62.3%; Score 127; DB 12; Length 103;  
Best Local Similarity 100.0%; Pred. No. 5.4e-10;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOEYKAMYAPPISQIR 24  
Db 51 KOIINMOEYKAMYAPPISQIR 74

RESULT 8  
078887 PRELIMINARY; PRT; 106 AA.  
AC 078887;  
DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)

DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE ENVELOPE POLYPROTEIN (FRAGMENT).  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=5990;  
RA Ou C.Y., Kalish M.;  
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.  
DR EMBL: L07161; AAB06861.1; -  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW Polypeptide; Envelope protein.  
FT NON\_TER 1  
FT SEQUENCE 106 AA: 11522 MW: B3ACDB26DB1390D2 CRC64;  
SQ

Query Match 62.3%; Score 127; DB 12; Length 106;  
Best Local Similarity 100.0%; Pred. No. 5.6e-10;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOEYKAMYAPPISQIR 24  
Db 51 KOIINMOEYKAMYAPPISQIR 74

RESULT 9  
073109 PRELIMINARY; PRT; 158 AA.  
AC 073109;  
DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98160778; PubMed=9499799;  
RA Shankarappa R., Gupta P., Learn G.H., Jr., Rodrigo A.G.,  
RA Rinaldo C.R., Jr., Gorry M.C., Millins J.I., Nara P.L., Enllich G.D.;  
RT "Evolution of human immunodeficiency virus type 1 envelope sequences  
RT in infected individuals with differing disease progression profiles";  
RL Virology 241:251-259(1998).  
DR EMBL: U15842; AAC59210.1; -  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT SEQUENCE 158 AA: 17521 MW: 005F9B3BAE1DAE93 CRC64;  
SQ

Query Match 62.3%; Score 127; DB 12; Length 158;  
Best Local Similarity 100.0%; Pred. No. 8.8e-10;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOEYKAMYAPPISQIR 24  
Db 114 KOIINMOEYKAMYAPPISQIR 137

RESULT 10  
073110 PRELIMINARY; PRT; 158 AA.  
AC 073110;  
DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).  
OC Human immunodeficiency virus type 1.  
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98160778; PubMed=9499799;  
RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G.,  
Rinaldo C.R. Jr., Gorry M.C., Millins J.I., Nara P.L., Ehrlich G.D.;  
RT "Evolution of human immunodeficiency virus type 1 envelope sequences  
in infected individuals with differing disease progression profiles.";  
RL Virology 241:251-259(1998).  
DR EMBL: U15845; AAC59153.1; -.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT TER 158  
SQ SEQUENCE 158 AA; 17551 MW; 0728EB3B4E184B93 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 158;  
Best Local Similarity 100.0%; Pred. No. 8.8e-10;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOWEYKAMYAPPISQIR 24  
Db 114 KOIINMOWEYKAMYAPPISQIR 137

RESULT 11  
073111 PRELIMINARY: PRT; 158 AA.  
AC 073111;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98160778; PubMed=9499799;  
RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G.,  
Rinaldo C.R. Jr., Gorry M.C., Millins J.I., Nara P.L., Ehrlich G.D.;  
RT "Evolution of human immunodeficiency virus type 1 envelope sequences  
in infected individuals with differing disease progression profiles.";  
RL Virology 241:251-259(1998).  
DR EMBL: U15844; AAC59152.1; -.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT TER 158  
SQ SEQUENCE 158 AA; 17551 MW; 0728EB3B4E184B93 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 158;  
Best Local Similarity 100.0%; Pred. No. 8.8e-10;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOWEYKAMYAPPISQIR 24  
Db 114 KOIINMOWEYKAMYAPPISQIR 137

RESULT 12  
073112 PRELIMINARY: PRT; 158 AA.  
AC 073112;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).  
OC Human immunodeficiency virus type 1.  
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98160778; PubMed=9499799;  
RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G.,  
Rinaldo C.R. Jr., Gorry M.C., Millins J.I., Nara P.L., Ehrlich G.D.;  
RT "Evolution of human immunodeficiency virus type 1 envelope sequences  
in infected individuals with differing disease progression profiles.";  
RL Virology 241:251-259(1998).  
DR EMBL: U15845; AAC59153.1; -.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT TER 158  
SQ SEQUENCE 158 AA; 17551 MW; 0728EB3B4E184B93 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 158;  
Best Local Similarity 100.0%; Pred. No. 8.8e-10;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOWEYKAMYAPPISQIR 24  
Db 114 KOIINMOWEYKAMYAPPISQIR 137

RESULT 13  
073113 PRELIMINARY: PRT; 158 AA.  
AC 073113;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98160778; PubMed=9499799;  
RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G.,  
Rinaldo C.R. Jr., Gorry M.C., Millins J.I., Nara P.L., Ehrlich G.D.;  
RT "Evolution of human immunodeficiency virus type 1 envelope sequences  
in infected individuals with differing disease progression profiles.";  
RL Virology 241:251-259(1998).  
DR EMBL: U15846; AAC59154.1; -.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT TER 158  
SQ SEQUENCE 158 AA; 17551 MW; 0728EB3B4E184B93 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 158;  
Best Local Similarity 100.0%; Pred. No. 8.8e-10;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMOWEYKAMYAPPISQIR 24  
Db 114 KOIINMOWEYKAMYAPPISQIR 137

RESULT 14  
073114 PRELIMINARY: PRT; 158 AA.  
AC 073114;

DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98160778; PubMed=9499799;  
 RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G.,  
 RA Rinaldo C.R., Gorry M.C., Millins J.I., Nara P.L., Ehrlich G.D.;  
 RT "Evolution of human immunodeficiency virus type 1 envelope sequences  
 in infected individuals with differing disease progression profiles.";  
 RL Virology 241:251-259(1998).  
 DR EMBL: U15847; AAC59155.1; -  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 FT NON\_TER 158  
 SQ SEQUENCE 158 AA; 17551 MW; 0728EB3B4E184B93 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-10;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMDEVGKAMYAPPISQIR 24  
 Db 114 KOIINMDEVGKAMYAPPISQIR 137

RESULT 15  
 ID 073107 PRELIMINARY; PRI; 160 AA.  
 AC 073107.  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN V3-V5 LOOP REGION (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98160778; PubMed=9499799;  
 RA Shankarappa R., Gupta P., Learn G.H. Jr., Rodrigo A.G.,  
 RA Rinaldo C.R., Gorry M.C., Millins J.I., Nara P.L., Ehrlich G.D.;  
 RT "Evolution of human immunodeficiency virus type 1 envelope sequences  
 in infected individuals with differing disease progression profiles.";  
 RL Virology 241:251-259(1998).  
 DR EMBL: U15840; AAC59208.1; -  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 FT NON\_TER 160  
 SQ SEQUENCE 160 AA; 17688 MW; DE195014562383A9 CRC64;

Query Match 62.3%; Score 127; DB 12; Length 160;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-10;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOIINMDEVGKAMYAPPISQIR 24  
 Db 116 KOIINMDEVGKAMYAPPISQIR 139

Search completed: January 2, 2002, 09:58:28  
 JobTime: 118 sec

Wed Jan 2 10:00:39 2002

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